

091712819

GenCore version: 5.1.6
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DM protein - protein search, using sw model

Run on: October 4, 2003, 12:17:36 : Search time 20.3333 seconds
(without alignments):
33.107 Million cell updates/sec

Title: US-09-712-819c-1
Perfect score: 32
Sequence: 1 FLT1SS 7
Scoring table: BLOSUM62
Gapcp 10.0 , Gapext 0.5

Searched: 283308 seqs, 96166692 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	54	2 JT0521	Ig kappa chain V-I
2	32	100.0	71	2 S21526	Ig kappa chain V r
3	32	100.0	77	2 D30502	Ig kappa chain V r
4	32	100.0	77	2 S70443	Ig kappa chain V r
5	32	100.0	78	2 S34102	Ig kappa chain V r
6	32	100.0	79	2 S24215	Ig kappa chain V r
7	32	100.0	81	2 PH1046	Ig light chain V r
8	32	100.0	83	2 S78489	Ig kappa chain V r
9	32	100.0	84	2 S34099	Ig kappa chain V r
10	32	100.0	86	2 S16626	Ig kappa chain V r
11	32	100.0	86	2 S16834	Ig kappa chain V r
12	32	100.0	86	2 S16836	Ig kappa chain V r
13	32	100.0	86	2 S34086	Ig kappa chain V r
14	32	100.0	86	2 S16340	Ig kappa chain V r
15	32	100.0	86	2 S16837	Ig kappa chain V r
16	32	100.0	86	2 S16833	Ig kappa chain V r
17	32	100.0	86	2 S16830	Ig kappa chain V r
18	32	100.0	86	2 S16824	Ig kappa chain V r
19	32	100.0	86	2 S16829	Ig kappa chain V r
20	32	100.0	87	2 S34098	Ig kappa chain V r
21	32	100.0	87	2 S21523	Ig kappa chain V r
22	32	100.0	87	2 S34037	Ig kappa chain V r
23	32	100.0	87	2 S34084	Ig kappa chain V r
24	32	100.0	87	2 S34083	Ig kappa chain V r
25	32	100.0	88	2 S21528	Ig kappa chain V r
26	32	100.0	88	2 S21525	Ig kappa chain V r
27	32	100.0	88	2 S21520	Ig kappa chain V r
28	32	100.0	88	2 S21522	Ig kappa chain V r
29	32	100.0	89	2 S34104	Ig kappa chain V r

Ig light chain V r
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r
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Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r

ALIGNMENTS

RESULT 1

JT0521
Ig kappa chain V-III region (CPI) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 00-May-1997
C/Accession: JT0521
R/Anker, R.; Conley, M.E.; Pollok, B.A.
R/Exp. Med. 169, 2109-2119, 1989
A/Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia
A/Reference number: JT0511; PMID:89279157; PMID:2785547
A/Accession: JT0521
A/Molecule type: mRNA
A/Residues: 1-54 <ANK>
A/Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangements
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-49/Domain: V region <VRE>
F/50-54/Domain: J region <JRE>

Query Match 100.0%; Score 32; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLT1SS 7
Db 23 FLT1SS 29

RESULT 2

S21526
Ig kappa chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 23-Jul-1999
C/Accession: S34082; S21526
R/Wagner, S.D.; Buzzatto, L.
R/Eur. J. Immunol. 23, 391-397, 1993
A/Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed in a clonal fashion
A/Reference number: S34076; PMID:93170387; PMID:8436174
A/Accession: S34082
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-71 <WA2>
A/Cross-references: EMBL:X66042; NID:G33318; PIDN:CAA46841.1; PID:G33319
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLT1SS 7
Db 23 FLT1SS 29

Db 64 FTLTSS 70

RESULT 3

D30502
Ig kappa chain V region (D44) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Nov-1988 #sequence_revision 33-Aug-1992 #text_change 23-Jul-1999
C:Accession: D30502
R:Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice
A:Reference number: A30502; NUID:88315787; PMID:2457627
A:Accession: D30502
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-77 <EIL>
A:Cross-references: GB:X21908; NID:g197073; PIDN:AAA9908.1; PID:g197074
A:Note: the authors translated the codon CAG for residue 48 as Pro
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 77;

Best Local Similarity 100.0%; Pred. No. 2.3;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7

Db 40 FTLTSS 46

RESULT 4

S70443
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 07-May-1999
C:Accession: S70443
R:Cuisinier, A.N.; Fumoux, F.; Fougereau, M.; Tanneille, C.
Vol. Immunol. 29, 1363-1373, 1992
A:Title: IGM kappa/lambda ESV human B cell clone: an early step of differentiation of B
A:Reference number: S70442; MUID:93024503; PMID:11395695
A:Accession: S70443
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-77 <CUI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 100.0%; Score 32; DB 2; Length 77;

Best Local Similarity 100.0%; Pred. No. 2.3;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7

Db 40 FTLTSS 46

RESULT 5

S34102
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999
C:Accession: S34102
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:91170387; PMID:8436174
A:Accession: S34102
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-78 <WAG>
A:Cross-references: EMBL:X67186
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 76;

Best Local Similarity 100.0%; Pred. No. 2.3;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7

Db 62 FTLTSS 60

RESULT 6

S24215
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24215
R:Shimizu, T.; Iwasato, T.; Yamagishi, H.
J. Exp. Med. 173, 1065-1072, 1991
A:Title: Deletions of immunoglobulin C(Kappa) region characterized by the circular exc
A:Reference number: S24214; MUID:91217618; PMID:1902500
A:Accession: S24215
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-79 <SHI>
A:Cross-references: EMBL:X58202; NID:g53718; PIDN:CAA4178.1; PID:g930195
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 79;

Best Local Similarity 100.0%; Pred. No. 2.3;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7

Db 44 FTLTSS 50

RESULT 7

Phi048
Ig light chain V region (clone 165.49) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: Phi048
R:Tillmar, D.M.; Jou, N.T.; Hill, R.J.; Mariott, T.N.
J. Exp. Med. 176, 765-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective f
A:Reference number: PH0371; MUID:92381444; PMID:11912540
A:Accession: Phi048
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-81 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 81;

Best Local Similarity 100.0%; Pred. No. 2.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7

Db 56 FTLTSS 62

RESULT 8

S78489
Ig kappa chain V region (patient 28) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000
C:Accession: S78489; S34100
R:Wagner, S.
Submitted to the EMBL Data Library, July 1992
A:Reference number: S78488

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A;Accession: S78485
A;Molecule type: DNA
A;Residues: 1-83 <WAG>
A;Cross-references: EXBL:X67184
A;Experimental source: patient 28
A;R;R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34100
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-88, 70-73, 75-83 <WAG>
A;Cross-references: EXBL:X67184
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
Db 61 FTLTSS 67

RESULT 9
S34099
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34099
A;R;R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34099
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-84 <WAG>
A;Cross-references: EXBL:X67183
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-79/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
Db 60 FTLTSS 66

RESULT 10
S34826
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16826; S34101
A;R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)II: variable regions of polyclonal rheumatoid f
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16826
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BIA>
A;Cross-references: EXBL:X54824; PID:G33654
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
Db 62 FTLTSS 68

RESULT 11
S16834
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16834
A;R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)II: variable regions of polyclonal rheumatoid f
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16834
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BIA>
A;Cross-references: EXBL:X54832
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
Db 62 FTLTSS 68

RESULT 12
S16836
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16836
A;R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)II: variable regions of polyclonal rheumatoid f
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16836
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BIA>
A;Cross-references: EXBL:X54834
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
Db 62 FTLTSS 68
```

C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 3;

Qy 1 FTLTSS 7
 |||||
 Db 62 FTLTSS 68

Search completed: October 4, 2003, 12:26:21
 Job time : 21.3333 secs

RESULT 13

S16837
 Ig kappa chain V region - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S16837
 R:Wagner, S.D.; Luzzatto, L.
 Eur. J. Immunol. 23, 391-397, 1993
 A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
 A:Reference number: S16837; PMID:8436174
 A:Accession: S16837
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-86 <BLA>
 C:Cross-references: EMBL:X54838
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
 |||||
 Db 64 FTLTSS 70

RESULT 14

S16840
 Ig kappa chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S16840
 R:Blaison, G.; Kuntz, J.L.; Pasquali, J.B.
 Eur. J. Immunol. 21, 1221-1227, 1991
 A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
 A:Reference number: S16840; PMID:1903706
 A:Accession: S16840
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-86 <BLA>
 C:Cross-references: EMBL:X54838
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
 |||||
 Db 62 FTLTSS 68

RESULT 15

S16837
 Ig kappa chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S16837
 R:Blaison, G.; Kuntz, J.L.; Pasquali, J.B.
 Eur. J. Immunol. 21, 1221-1227, 1991
 A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
 A:Reference number: S16837; PMID:1903706
 A:Accession: S16837
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-86 <BLA>
 C:Cross-references: EMBL:X54838

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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:09:51 ; Search time 10.6667 Seconds
(without alignments)
30.962 Million cell updates/sec

Title: us-09-712-819c-1

Perfect score: 32
Sequence: 1 FTLTISS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapex: 0.5

Searched: 127861 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	107	1 KV1D_HUMAN	P01596 homo sapien
2	32	100.0	108	1 KV1F_HUMAN	P01598 homo sapien
3	32	100.0	108	1 KV1G_HUMAN	P01599 homo sapien
4	32	100.0	108	1 KV1H_HUMAN	P01600 homo sapien
5	32	100.0	108	1 KV1S_HUMAN	P01611 homo sapien
6	32	100.0	108	1 KV5Q_MOUSE	P01650 mus musculus
7	32	100.0	108	1 KV5R_MOUSE	P01651 mus musculus
8	32	100.0	108	1 KV5S_MOUSE	P01652 mus musculus
9	32	100.0	108	1 KV5T_MOUSE	P01653 mus musculus
10	32	100.0	109	1 KV1T_HUMAN	P01612 homo sapien
11	32	100.0	109	1 KV3F_HUMAN	P01624 homo sapien
12	32	100.0	114	1 KV1A_MOUSE	P01632 mus musculus
13	32	100.0	114	1 KV4A_HUMAN	P01625 homo sapien
14	32	100.0	115	1 KV3I_HUMAN	P04433 homo sapien
15	32	100.0	116	1 KV3J_HUMAN	P04434 homo sapien
16	32	100.0	117	1 KV1I_HUMAN	P01601 homo sapien
17	32	100.0	117	1 KV1O_HUMAN	P01602 homo sapien
18	32	100.0	121	1 KV4O_HUMAN	P06312 homo sapien
19	32	100.0	129	1 KV1W_HUMAN	P04431 homo sapien
20	32	100.0	129	1 KV1X_HUMAN	P04432 homo sapien
21	32	100.0	133	1 KV4B_HUMAN	P06113 homo sapien
22	32	100.0	134	1 KV4C_HUMAN	P06114 homo sapien
23	32	100.0	136	1 KV5B_MOUSE	P01634 mus musculus
24	30	93.8	354	1 OPS1_ASTFA	P51474 asyana fa
25	29	90.6	108	1 KV1L_HUMAN	P01604 homo sapien
26	29	90.6	108	1 KV1Q_HUMAN	P01639 homo sapien
27	29	90.6	108	1 KV1R_HUMAN	P01610 homo sapien
28	29	90.6	400	1 CN37_BOVIN	P06623 bos taurus
29	29	90.6	421	1 CN37_HUMAN	P09543 homo sapien
30	28	87.5	92	1 KV09_RABIT	P01590 oryctolagus
31	28	87.5	100	1 KV3C_HUMAN	P01621 homo sapien
32	28	87.5	104	1 KV17_RABIT	P01698 oryctolagus
33	29	87.5	107	1 KV04_RABIT	P01685 oryctolagus

34 28 87.5 108 1 KV35_RABIT P01686 oryctolagus
35 28 87.5 108 1 KV06_RABIT P01687 oryctolagus
36 28 87.5 108 1 KV07_RABIT P01688 oryctolagus
37 28 87.5 108 1 KV08_RABIT P01689 oryctolagus
38 28 87.5 108 1 KV1B_HUMAN P01594 homo sapien
39 28 87.5 108 1 KV1E_HUMAN P01597 homo sapien
40 28 87.5 108 1 KV1K_HUMAN P01603 homo sapien
41 28 87.5 108 1 KV1X_HUMAN P01605 homo sapien
42 28 87.5 108 1 KV1N_HUMAN P01606 homo sapien
43 28 87.5 108 1 KV1P_HUMAN P01608 homo sapien
44 28 87.5 108 1 KV1Y_HUMAN P00162 homo sapien
45 28 87.5 108 1 KV1A_HUMAN P01619 homo sapien

ALIGNMENTS

RESULT 1
KV1D_HUMAN
ID "KV1D_HUMAN STANDARD; PRT; 107 AA.
AC P01596; 1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
ST 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-I region CAR.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75075135; PubMed=4216454;
RA Maltstein C.P., Deverson E.V.;
RT "Primary structure of kappa light chain from a human myeloma protein."
RL Eur. J. Biochem. 49:377-391(1974).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A01864; K1HJAR.
DR HSP: P83362; IWTL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; F:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR0031006; IG_MHC.
DR InterPro: IPR0031596; IG_v.
DR Pfam: PF000047; ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 FTLTISS 7
Db 71 FTLTISS 77

RESULT 2
KV1F_HUMAN
ID "KV1F_HUMAN STANDARD; PRT; 108 AA.
AC P01598; 1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
ST 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-I region EU.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=7064023; PubMed=549770;
 RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.,
 RT "The covalent structure of a human gamma G-immunoglobulin. V. Amino
 RT acid sequence of the light chain."
 RT Biochemistry 9:3155-3161(1970).
 RN [2]
 RP DISULFIDE BOND.
 RX MEDLINE=71064027; PubMed=4923144;
 RA Gal, W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 RT Intrachain disulfide bonds."
 RT Biochemistry 9:3148-3156(1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 CC PIR; A90562; KIHJEU.
 DR HSSP; P01607; IREI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11788 MW; 9CD2942F4D88623 CRC64;
 Query Match 100.0%; Score 32; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.93;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FILTISS 7
 DB 71 FILTISS 77

RESULT 3
 KVIG_HUMAN STANDARD; PRT; 108 AA.
 ID KVIG_HUMAN
 AC P01599;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-1 region Gal.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=7059122; PubMed=4215718;
 RA Laure C.O., Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal IgM-immunoglobulin
 RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
 RT kappa-type, subgroup I."
 RT Hoppe-Sevler's Z. Physiol. Chem. 354:1503-1504(1973).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S

MACROGLOBULIN.
 DR PIR; A01967; KIHUGL.
 DR HSSP; P01607; IREI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11814 MW; C1A03CB3F600FF73 CRC64;
 Query Match 100.0%; Score 32; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.93;
 Matches 7; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
 QY 1 FILTISS 7
 DB 71 FILTISS 77

RESULT 4
 KVIG_HUMAN STANDARD; PRT; 108 AA.
 ID KVIG_HUMAN
 AC P01606;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-1 region Hau.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=7032830; PubMed=4097974;
 RA Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
 RT chain of subgroup I (Bence-Jones Protein Hau); subdivision within
 RT subgroups."
 RT Hoppe-Sevler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01868; KIHCHU.
 DR HSSP; P80362; IWTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97

```

FTT DOMAIN 38 107 FRAMEWORK-4.
FTT DISULFID 23 98 BY SIMILARITY.
FTT NON TER 108 108
SSQ SEQUENCE 108 AA; 11671 MW; C8D3A516CF80C618 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
DB 71 FTLTSS 77

RESULT 5
MEDLINE=81092279; PubMed=6778806;
Kratz H., Yang C., Krusche J.J., Hilschmann N.;
"Preparative separation of the tryptic hydrolysate of a protein by
high-pressure liquid chromatography. The primary structure of a
monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
Wes).";
Hoppe-Seyler's Z. Physikl. Chem. 361:1531-1598 (1980).
-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR: A01877; KIHWS.
HSSP: P80362; IWTU.
GO: GO:0005576; C:extracellular; NAS.
GO: GO:0003823; P:antigen binding activity; NAS.
GO: GO:0006955; P:immune response; NAS.
InterPro: IPR007110; IG-like.
InterPro: IPR003006; IG_MHC.
InterPro: IPR003596; IG_V.
Pfam: PF00047; IG_1.
SMART: SM00406; IGV; 1.
PROSITE: PS00835; IG_LIKE; 1.
Immunoglobulin V region; Bence-Jones protein.
DOMAIN 1 23 FRAMEWORK-1.
DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
DOMAIN 35 49 FRAMEWORK-2.
DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
DOMAIN 57 88 FRAMEWORK-3.
DOMAIN 89 97 FRAMEWORK-4.
DOMAIN 96 107 COMPLEMENTARITY-DETERMINING-3.
DISULFID 23 88 BY SIMILARITY.
NON TER 108 108
SEQUENCE 108 AA; 11608 MW; 782B14A649A63E45 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
DB 71 FTLTSS 77

RESULT 6
MEDLINE=79195288; PubMed=109517;
Vrana M., Radikoff S., Potter M.;
"The structural basis of a hapten-inhibitable kappa-chain idiotype.";
J. Immunol. 122:1905-1910 (1979).
-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
BIND BETA(2-1)-FRUCTOFURANOSYL MOETIES (INULIN).
PIR: B92808; KWS09.
HSSP: P01607; IREI.
InterPro: IPR007110; IG-like.
InterPro: IPR003006; IG_MHC.
InterPro: IPR003596; IG_V.
Pfam: PF00047; IG_1.
SMART: SM00406; IGV; 1.
PROSITE: PS00835; IG_LIKE; 1.

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region UPC 61.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79195288; PubMed=109517;
RA Vrana M., Radikoff S., Potter M.;
R: "The structural basis of a hapten-inhibitable kappa-chain idiotype.";
J. Immunol. 122:1905-1910 (1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
BIND BETA(2-1)-FRUCTOFURANOSYL MOETIES (INULIN).
CC PIR: B92808; KWS09.
DR HSSP: P80362; IWTU.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11809 MW; FAE4DA36076F2AFE CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
DB 71 FTLTSS 77

RESULT 7
MEDLINE=79195288; PubMed=109517;
Vrana M., Radikoff S., Potter M.;
"The structural basis of a hapten-inhibitable kappa-chain idiotype.";
J. Immunol. 122:1905-1910 (1979).
-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
BIND BETA(2-1)-FRUCTOFURANOSYL MOETIES (INULIN).
PIR: B92808; KWS09.
DR HSSP: P01607; IREI.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.

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KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 98 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11876 MW; 35C116B360F79310 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
Db 71 FTLTSS 77

RESULT 8
KV55 MOUSE
ID KV55 MOUSE STANDARD; PRT; 108 AA.
AC P01652;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region J666.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
binding proteins."
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR PIR; A92811; KMS26.
DR HSSP; P016C7; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SMC0406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 98 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11850 MW; C5C145DC376F30CE CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
Db 71 FTLTSS 77

RESULT 10
KV17 HUMAN
ID KV17 HUMAN STANDARD; PRT; 109 AA.
AC P01612;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-I region Mev.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83081018; PubMed=6816713;
RA Eulitz M., Linke R.P.;
RT "Primary structure of the variable part of an amyloidogenic
Bence-Jones Protein (Mev). An unusual insertion in the third
hypervariable region of a human kappa-immunoglobulin light chain."
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1347-1359(1982).
CC -!- MISCELLANEOUS: ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO
CC FOUND.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01879; KIHUMV.
DR HSSP; P80362; 1WTL.
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DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; P:antigen binding activity; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG-MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG-LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein.
KW DOMAIN 24 34
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 98
FT DOMAIN 99 98
FT DOMAIN 99 138
FT DISULFID 23 88
FT NON_TER 139 139
SQ SEQUENCE 109 AA; 11876 MW; B6APF451D5F5A0 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 109;

Best Local Similarity 100.0%; Pred. No. 0.94; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Indels 0; Gaps 0;

RESULT 11

ID KV3F HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE IG kappa chain V-III region POM.
DS Homo sapiens (Human).
DC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
from two idiotypically cross reactive IGM anti-gamma globulins";
RT Ann. Immunol. (Paris) 127C:261-271(1976).
SC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.
CC PIR; A01897; K3HUPM.
DR HSSP; P00362; IWTL.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; P:antigen binding activity; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG-MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A6A86A86 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 109;

Best Local Similarity 100.0%; Pred. No. 0.94; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Indels 0; Gaps 0;

Db 72 FTLTSS 78

RESULT 12

ID KV1A MOUSE STANDARD; PRT; 114 AA.
AC P01632;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-I region SIC7A.
CS Mus musculus (Mouse).
OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=81241357; PubMed=678869C;
RA Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Scharff M.D.;
RT "Nucleic acid and protein sequences of phosphocholine-binding light
chains";
RL J. Exp. Med. 153:1366-1370(1981).
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL; U29423; AAC00033.1; -

DR FTR; A01915; KVM57A.

DR HSSP; P01607; IREI.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003006; IG-MHC.

DR InterPro: IPR003596; IG_V.

DR Pfam: PF00047; IG; 1.

DR SMART: SM00406; IGV; 1.

DR PROSITE: PS00835; IG-LIKE; 1.

KW Immunoglobulin V region.

FT DOMAIN 1 23

FT DOMAIN 24 40

FT DOMAIN 41 55

FT DOMAIN 56 62

FT DOMAIN 63 94

FT DOMAIN 95 103

FT DOMAIN 104 113

FT DISULFID 23 94

FT NON_TER 114 114

SQ SEQUENCE 114 AA; 12717 MW; 32008EC8E9DBE67B CRC64;

Query Match 100.0%; Score 32; DB 1; Length 114;

Best Local Similarity 100.0%; Pred. No. 0.99; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7

Db 77 FTLTSS 83

RESULT 13

ID KV4A HUMAN STANDARD; PRT; 114 AA.
AC P01625;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG kappa chain V-IV region Len.
CS Homo sapiens (Human).
OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;

RN SEQUENCE.
 RX MEDLINE=76004342; PubMed:50955;
 RA Schneider M., Hilschmann N.,
 RT "The primary structure of a monoclonal immunoglobulin-L-chain of
 RL subgroup IV of the kappa type (Bence-Jones protein Ben1)."
 RN Hoppe-Seyler's Z. Physiol. Chem. 356:507-557 (1975).
 RP REVISION TO 9.
 RA Salomon A.,
 RL Submitted (AUG-1986) to the SWISS-PROT data bank.
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PDB; 1EEQ; 01-FEB-01.
 DR PDB; 1EEU; 03-FEB-01.
 DR PDB; 1EFQ; 09-FEB-01.
 DR PDB; 1EX3; 06-MAR-01.
 DR PDB; 1LVE; 21-JAN-98.
 DR PDB; 3LVE; 18-MAY-99.
 DR PDB; 5LVE; 28-MAR-01.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 41 55 FRAMEWORK-2.
 FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 63 94 FRAMEWORK-3.
 FT DOMAIN 95 101 FRAMEWORK-4.
 FT DOMAIN 102 113 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 94 BY SIMILARITY.
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17236485 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 114;
 Best Local Similarity 100.0%; Prod. No. 599;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY : FTLTSS 7
 DB 77 FTLTSS 81
 RESULT 14
 KV31 HUMAN STANDARD; PRT; 115 AA.
 ID KV31 HUMAN
 AC PC4453;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region VG precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 ON NCBI_TaxID=9606;
 RN SEQUENCE FROM N.A.
 RX MEDLINE=85087932; PubMed=6440122;
 RA Pech M., Zachau H.G.;
 RT "Immunoglobulin genes of different subgroups are interdigitated
 within the VK locus."
 RL Nucleic Acids Res. 12:9229-9236 (1984).
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; XC2725; -; NOT ANNOTATED_CDS.
 DR PIR; A01501; K3HUVH.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.

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 CC -----
 DR EMBL; X01668; -; NOT ANNOTATED_CDS.
 DR PIR; A01900; K3HUVG.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 69 FRAMEWORK-2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 77 108 FRAMEWORK-3.
 FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;
 Query Match 100.0%; Score 32; DB 1; Length 115;
 Best Local Similarity 100.0%; Prod. No. 1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY : FTLTSS 7
 DB 91 FTLTSS 97
 RESULT 15
 KV31 HUMAN STANDARD; PRT; 116 AA.
 ID KV31 HUMAN
 AC P04434;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region VG precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 ON NCBI_TaxID=9606;
 RN SEQUENCE FROM N.A.
 RX MEDLINE=85087932; PubMed=6440122;
 RA Pech M., Zachau H.G.;
 RT "Immunoglobulin genes of different subgroups are interdigitated
 within the VK locus."
 RL Nucleic Acids Res. 12:9229-9236 (1984).
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; XC2725; -; NOT ANNOTATED_CDS.
 DR PIR; A01501; K3HUVH.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003536; IG_v.
DR Zfam: PF00647; ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION VH.
FT DOMAIN 21 42 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 119 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12757 MW; 51CD558A53B21929 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLTSS 7
Db 92 FTLTSS 98

Search completed: October 4, 2003, 12:22:36
Job time : 11.6667 secs

GenCore version 5.1.6
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DM protein - protein search, using sw model

Run on: October 4, 2003, 12:17:13 : Search time 49.6667 Seconds
(without alignments)
36.370 Million cell updates/sec

Title: US-09-712-819c-1

Perfect score: 32

Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 81525 seqs, 254552604 residues

Total number of hits satisfying chosen parameters: 81525

Minimum DB seq length: 3

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mmc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_todent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	32	100.0	107	4 Q96SA9	Q96SA9 homo sapien
2	32	100.0	107	1: Q9ER29	Q9ER29 mus musculu
3	32	100.0	106	4 Q9UL83	Q9UL83 homo sapien
4	32	100.0	108	4 Q9UL70	Q9UL70 homo sapien
5	32	100.0	108	4 Q9UL77	Q9UL77 homo sapien
6	32	100.0	109	4 Q9UL85	Q9UL85 homo sapien
7	32	100.0	234	4 Q9NEK1	Q9NEK1 homo sapien
8	30	93.8	320	16 Q8FFC5	Q8FFC5 escherichia
9	30	93.8	378	5 Q8MZH9	Q8MZH9 drosophila
10	30	93.8	1004	7 Q28412	Q28412 archaeglob
11	29	90.6	108	1: Q8V1C0	Q8V1C0 mus musculu
12	29	90.6	116	4 Q96FF6	Q96FF6 homo sapien
13	29	90.6	168	16 Q8YLX8	Q8YLX8 anabaena sp
14	29	90.6	171	12 Q69504	Q69504 human hepa
15	29	90.6	195	12 Q9JCS8	Q9JCS8 rice tungro
16	29	90.6	195	12 Q9JCS0	Q9JCS0 rice tungro

ALIGNMENTS

RESULT :

Q96SA9 PRELIMINARY; PRT; 107 AA.

ID Q96SA9; AC Q96SA9; CT 01-DEC-2001 (TREMBL:rel. 19, Created)
CT 01-DEC-2001 (TREMBL:rel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBL:rel. 23, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic arthritis: human anti-N-acetylglucosamine/anti-myosin
RT antibody v region genes";
RJ J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SMC0406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 4B343E9C5B577F16 CRC64;

Query Match 100.0%; Score 32; DB 4; Length 107;

Best Local Similarity 100.0%; Pred.No. 7;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FTLTSS 7

Db 71 FTLTSS 77

RESULT 2

```
Q9ERZ9
ID Q9ERZ9 PRELIMINARY; PRT; 107 AA.
AC Q9ERZ9
DT 01-MAR-2003 (TrEMBLrel. 16, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti human TNF-alpha light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN [2]
SEQUENCE FROM N.A.
Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
"Construction and sequencing of the single-chain antibody gene of a
human TNF-alpha specific monoclonal antibody.";
J Cell. Mol. Immunol. 12:21-26(1996).
[3]
SEQUENCE FROM N.A.
Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
EMBL; AF262753; AAG23804.1; -.
DR HSSP; P8C362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003066; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER 107
SQ SEQUENCE 107 AA; 11784 MW; 2B5EEA6604A26C3 CRC64;
```

```
Query Match 100.0%; Score 32; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. NC. 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
DB 74 FTLTSS 60
```

RESULT 3

```
Q9JL83
ID Q9JL83 PRELIMINARY; PRT; 108 AA.
AC Q9JL83
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN [2]
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EXBL; AF035031; AAG25676.1; -.
DR HSSP; P80362; 1WTL.
```

```
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003066; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F0C5A92E5A96EEA CRC64;

Query Match 100.0%; Score 32; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. NC. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
DB 71 FTLTSS 77
```

RESULT 4

```
Q9JL70
ID Q9JL70 PRELIMINARY; PRT; 108 AA.
AC Q9JL70
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EXBL; AF035044; AAG56280.1; -.
DR HSSP; P81607; 1REI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003066; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCA37 CRC64;
```

```
Query Match 100.0%; Score 32; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. NC. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
DB 71 FTLTSS 77
```

RESULT 5

```
Q9JL77
ID Q9JL77 PRELIMINARY; PRT; 108 AA.
AC Q9JL77
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```

DX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RRL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EVBL; AF035037; AAD56273.1; --
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR NON_TER 1
DR NON_TER 108
DR SEQUENCE 108 AA; 11738 MW; C36681716C4D16F3 CRC64;

Query Match 100.0%; Score 32; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 7.1; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

ay 1 FTLTSS 7
b 71 FTLTSS 77

RESULT 6
Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
NS Homo sapiens (Human).
NC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RRL Clin. Immunol. Immunopathol. 97:184-192(1998).
DR EVBL; AF035029; AAD56265.1; --
DR HSSP; P80362; IWTJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR NON_TER 1
DR NON_TER 109
DR SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 100.0%; Score 32; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 7.2; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

ay 1 FTLTSS 7
b 71 FTLTSS 77

RESULT 7

```

```

Q8NEK1 PRELIMINARY; PRT; 234 AA.
AC Q8NEK1;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
CS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBRC databases.
DR EVBL; BC035813; AAH30813.1; --
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25530 MW; 6316E3DEFF8D132F8 CRC64;

Query Match 100.0%; Score 32; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 15; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

ay 1 FTLTSS 7
b 91 FTLTSS 97

RESULT 8
Q8FFC5 PRELIMINARY; PRT; 320 AA.
AC Q8FFC5;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein yfen.
GN YFEN OR C2941
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
CC NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=06:HI / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Rackett J., Strode D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RRL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EVBL; AF016764; AAN81391.1; --
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 320 AA; 37039 MW; EEB33B2B2E3811DF CRC64;

Query Match 93.8%; Score 30; DB 16; Length 320;
Best Local Similarity 85.7%; Pred. No. 61; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0;

ay 1 FTLTSS 7
b 72 FTLTSS 78

RESULT 9

```



```

DR EMBL; AF361759; AAK51465.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
DR NON_TER 1
FT NON_TER 116
FT SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;
SQ
Query Match 90.6%; Score 29; DB 4; Length 116;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTSS 7
DB 71 FVTSS 77
RESULT 13
ID Q8YLY8 PRELIMINARY; PRT; 162 AA.
AC Q8YLY8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein A25156.
GN ALR3156.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
CC NCBI_TaxID=503690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kanketo T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashina K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2002).
DR EMBL; AF003598; BAB376855.1; -.
DR InterPro; IPR004919; DJF262.
DR Pfam; PF03235; DJP262; 1.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 168 AA; 19416 MW; 54D5A218A4886C1B CRC64;
Query Match 90.6%; Score 29; DB 16; Length 168;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTSS 7
DB 93 FTLTAS 99
RESULT 14
ID Q69504 PRELIMINARY; PRT; 171 AA.
AC Q69504;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE U23 protein.
GN U23.
OS Human herpesvirus (type 7 / strain J1) (HHV7);
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
XC Alphaherpesvirinae; Simplexvirus.
CC NCBI_TaxID=57278;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN=J1;
RA Nicholas J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RR;
RA Megaw A.G., Rapaport D., Avidor B., Frenkel N., Davison A.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=RR;
RA Megaw A.G., Frenkel N., Davison A.J.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; J43400; AAC54684.1; -.
DR EMBL; AF037218; AAC40736.1; -.
SQ SEQUENCE 171 AA; 18663 MW; ACB35FAS593D8C1C CRC64;
Query Match 90.6%; Score 29; DB 12; Length 171;
Best Local Similarity 85.7%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTSS 7
DB 98 FTLTST 104
RESULT 15
ID Q9JCS8 PRELIMINARY; PRT; 195 AA.
AC Q9JCS8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Coat protein 1 (Fragment).
GN CPL.
OS Rice tungro spherical virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Sequiviridae;
CC Maikavirus.
CC NCBI_TaxID=35287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PC88ii;
RA Azzam O.I., Yambao M.L.M., Muhsin M., McNally K.L., Umachay K.M.L.;
RT "Genetic diversity of rice tungro spherical virus in tungro-endemic
RT provinces of the Philippines and Indonesia."
RL Arch. Virol. 145:0-0(2000).
DR EMBL; AF223080; AAF65291.1; -.
FT NON_TER 1
FT NON_TER 195
FT SEQUENCE 195 AA; 20865 MW; 11B3D6D370445CD7 CRC64;
Query Match 90.6%; Score 29; DB 12; Length 195;
Best Local Similarity 85.7%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTSS 7
DB 74 FTLTTS 80
Search completed: October 4, 2003, 12:25:14
Job time : 51.6667 secs

```


PT reducing eosinophilia and for treating certain allergic diseases,
 PT esp. asthma
 XX Example 3; Fig 3; 69pp; English.
 CC Framework regions (AAR87041-44) of human group 1 (gpl) germ line
 CC antibody light chain showed homology to corresponding regions
 CC (AAR87045-48, respectively) of the rat anti-human interleukin-5
 CC monoclonal antibody 39D10 light chain (see AAR87040). This homology
 CC was utilised in the prodn. of a humanised 39D10 VL (AAR87057) in
 CC which rat 39D10 VL complementarity determining regions were grafted
 CC into the human gpl framework.
 XX
 XX Sequence 32 AA:
 SQ
 Query Match 100.0%; Score 32; DB 17; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 FTLTSS 7
 DB 15 FTLTSS 21
 RESULT 2
 AAY52745
 ID AAY52745 standard; Peptide; 32 AA.
 AC AAY52745;
 XX
 XX 26-JAN-2000 (first entry)
 XX Humanised ATR-5 L Chain V region FR3 for a.
 XX
 XX Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
 XX ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
 XX disseminated intravascular coagulation; immunogenicity; chimeric.
 XX
 XX Synthetic.
 XX Homo sapiens.
 XX W09951743-A1.
 XX 14-OCT-1999.
 XX
 XX 02-APR-1999; 99WO-JP01768.
 XX
 XX 03-APR-1999; 98JP-C091853.
 XX
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Sato K, Adachi H, Yabuta N;
 XX WPI; 1999-620204/53.
 XX
 XX Humanised antibody recognizing human tissue factor, used for treatment
 XX of disseminated intravascular coagulation.
 XX
 XX Claim 17; Page 270; 291pp; Japanese.
 XX
 XX The present invention describes chimeric antibody (Ab) heavy (H) chains
 XX containing the variable region of the H chain of a mouse monoclonal Ab
 XX recognising human tissue factor (HTF) and the constant region of the H
 XX chain of a human Ab. The variable region is one of six specified
 XX sequences (which are the H chain variable regions from mouse monoclonal
 XX Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L)
 XX chains containing the variable region of the L chain of a mouse
 XX monoclonal Ab recognising human tissue factor (HTF) and the constant
 XX region of the L chain of a human Ab, the variable region being one of six
 XX specified sequences (which are the L chain variable regions from mouse
 XX monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for
 XX the treatment and prevention of thrombotic disease, especially of
 XX disseminated intravascular coagulation (DIC). The humanised antibody has

CC the high HTF binding activity of the mouse monoclonal antibody but
 CC greatly reduced immunogenicity. AAZ33003 to AAZ33051 and Y527007 to
 CC AAY52767 represent sequences used in the exemplification of the present
 CC invention.
 XX
 XX Sequence 32 AA:
 SQ
 Query Match 100.0%; Score 32; DB 20; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 FTLTSS 7
 DB 15 FTLTSS 21
 RESULT 3
 AAB98286
 ID AAB98286 standard; Peptide; 32 AA.
 XX AAB98286;
 XX AAB98286;
 XX 20-AUG-2001 (first entry)
 XX Anti-A33 antigen immunoglobulin VL FR3 SEQ ID NO:92.
 XX Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
 XX immunoglobulin; complementarity determining region; CDR; cancer;
 XX cytostatic; anticancer; colon cancer; stomach cancer.
 XX Homo sapiens.
 XX W0200130393-A2.
 XX 03-MAY-2001.
 XX 20-OCT-2000; 2000WO-US29289.
 XX 22-OCT-1999; 99JS-0425638.
 XX 04-APR-2000; 2000US-0543004.
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX (SLOK) SLOAN KETTERING INST CANCER RES.
 XX (SCRI) SCRIPPS RES INST.
 XX Barbas CF, Rader C, Ritter G, Welt S, Old LJ;
 XX WPI; 2001-328613/34.
 XX Treating cancers, particularly of stomach and colon, that express A33
 XX antigen by administering conjugate of anticancer agent with specific
 XX immunoglobulin product.
 XX Claim 16; Page 40; 85pp; English.
 XX
 XX The present invention describes a method for treating cancers that
 XX express the A33 antigen. The method comprises administering an
 XX anticancer agent (I) conjugated to an immunoglobulin product (II) that
 XX binds specifically to A33 and contains one or more of 13 specified
 XX complementarity determining regions (CDRs), given in AAB98286 to
 XX AAB98274. (I) has cytostatic activity. The method can be used for
 XX treating colon and stomach cancers. (II), or the nucleic acid encoding
 XX it, can be used directly, in unconjugated form, for immunotherapy of
 XX cancer, and, when labeled, for detection or diagnosis of diseases
 XX associated with A33 expression. AAB22218 to AAB22254 and AAB98230 to
 XX AAB98321 represent sequences used in the exemplification of the
 XX present invention.
 XX
 XX Sequence 32 AA;
 SQ
 Query Match 100.0%; Score 32; DB 22; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 FTLTSS 7
Db      15 FTLTSS 21

RESULT 4
AA398288
ID AAB98288 standard; Peptide; 32 AA.
AC AAB98288;
XX
XX
XX 20-AUG-2001 (first entry);
DE
DE Anti-A33 antigen immunoglobulin VL FR3 SEQ ID NO:94.
XX
XX Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
XX immunoglobulin; complementarity determining region; CDR; cancer;
XX cytostatic; anticancer; colon cancer; stomach cancer.
XX
XX Homo sapiens.
OS
XX WO200130393-A2.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-US29289.
XX
XX 22-OCT-1999; 99US-0425638.
XX
XX 04-APR-2000; 2000US-0543004.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX (SLOK-) SLOAN KETTERING INST CANCER RES.
XX (SCRI-) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C, Weit S, Cld LG;
XX WPI; 2001-328613/34.
XX
XX Treating cancers, particularly of stomach and colon, that express A33
XX antigen by administering conjugate of anticancer agent with specific
XX immunoglobulin product -
XX
XX Claim 16; Page 40; 85pp; English.
XX
XX The present invention describes a method for treating cancers that
XX express the A33 antigen. The method comprises administering an
XX anticancer agent (i) conjugated to an immunoglobulin product (ii) that
XX binds specifically to A33 and contains one or more of i3 specified
XX complementarity determining regions (CDRs), given in AAB98262 to
XX AAB98274. (i) has cytostatic activity. The method can be used for
XX treating colon and stomach cancers. (ii), or the nucleic acid encoding
XX it, can be used directly, in unconjugated form, for immunotherapy of
XX cancer, and, when labeled, for detection or diagnosis of diseases
XX associated with A33 expression. AAH22218 to AAH22254 and AAB38230 to
XX AAB98321 represent sequences used in the exemplification of the
XX present invention.
XX
XX Sequence 32 AA;
XX
XX Query Match 100.0%; Score 32; DB 22; Length 32;
XX Best Local Similarity 100.0%; Pred. No. 4.6;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 FTLTSS 7
Db      15 FTLTSS 21

RESULT 5
AAB97666
ID AAB97666 standard; Peptide; 32 AA.
XX
XX
XX
XX 03-AUG-2001 (first entry);
XX
XX A33 antigen binding immunoglobulin product VLFR3 peptide SEQ ID NO:92.
XX
XX Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
XX immunoreact; anti A33 antigen antibody; immunoglobulin.
XX
XX Homo sapiens.
XX
XX WO200131065-A1.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-US29026.
XX
XX 22-OCT-1999; 99US-0425638.
XX
XX 04-APR-2000; 2000US-0543004.
XX
XX (SCRI-) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C;
XX WPI; 2001-328657/34.
XX
XX Preparing humanized rabbit antibodies that specifically immunoreact
XX with a particular antigen using display technology for expressing
XX libraries of antibody domains and fine tuning variable domain regions -
XX
XX Example 9; Page 39; 62pp; English.
XX
XX The present invention describes a method for preparing a humanised rabbit
XX antibody that specifically immunoreacts with a particular antigen. The
XX method comprises expressing a library of antibodies comprising one or
XX more complementarity determining region (CDR) from the variable domain
XX sequences that specifically immunoreact with the antigen grafted into
XX framework regions from humans, and selecting the antibodies that react
XX with the antigen. The method is useful for humanising non-human
XX mammalian antibodies, which can be used for the treatment of a variety
XX of diseases. The present sequence represents an A33 antigen binding
XX immunoglobulin product VLFR3 peptide which is given in an example from
XX the present invention.
XX
XX Sequence 32 AA;
XX
XX Query Match 100.0%; Score 32; DB 22; Length 32;
XX Best Local Similarity 100.0%; Pred. No. 4.6;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 FTLTSS 7
Db      15 FTLTSS 21

RESULT 6
AAB97668
ID AAB97668 standard; Peptide; 32 AA.
XX
XX
XX
XX 08-AUG-2001 (first entry)
XX
XX A33 antigen binding immunoglobulin product VLFR3 peptide SEQ ID NO:94.
XX
XX Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
XX immunoreact; anti A33 antigen antibody; immunoglobulin.
XX
XX Homo sapiens.
XX
XX WO200131065-A1.
XX
XX 03-MAY-2001.

```


PR 26-JAN-2001; 2001US-264451P.
 XX (SCRI) SCRIPPS RES INST.
 XX Maruyama T, Jones IM, Burton DR, Fox RI;
 PI WPI; 2002-599801/64.
 DR New human immunopolyptide with binding specificity for certain
 PT envelope glycoproteins and nonstructural proteins of hepatitis C virus
 PT (HCV), for diagnosing or treating patients having or suspected of
 PT having HCV infection -
 XX Claim 4; Fig 17; 308pp; English.
 XX The present invention relates to human immunopolyptides, produced by a
 CC phage transfect cell library. The present sequence is one such
 CC immunopolyptide. The immunopolyptides have binding specificity for
 CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
 CC virus (HCV). E2 glycoprotein is believed to be responsible for target
 CC cell binding and contains neutralising epitopes, while NS3 is thought to
 CC be involved in the replication of HCV. The immunopolyptides are useful
 CC for diagnosing and treating a patient having or suspected to be having
 CC HCV infection.
 XX Sequence 32 AA;
 SQ Query Match 100.0%; Score 32; DB 23; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTUTISS 7
 DB 15 FTUTISS 21

RESULT 9
 ABP62673
 ID ABP62673 standard; Peptide; 32 AA.
 AC ABP62673;
 XX 10-OCT-2002 (first entry)
 XX Human immunopeptide to HCV E2 glycoprotein framework sequence #181.
 DE Virucide; human; immunopolyptide; immunopeptide; envelope glycoprotein;
 KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
 KW NS3 protein; viral infection.
 XX Homo sapiens.
 OS WO200259340-A1.
 XX 01-AUG-2002.
 XX 25-JAN-2002; 2002WO-US02303.
 XX 26-JAN-2001; 2001US-264451P.
 XX (SCRI) SCRIPPS RES INST.
 XX Maruyama T, Jones IM, Burton DR, Fox RI;
 XX WPI; 2002-599801/64.
 XX New human immunopolyptide with binding specificity for certain
 PT envelope glycoproteins and nonstructural proteins of hepatitis C virus
 PT (HCV), for diagnosing or treating patients having or suspected of
 PT having HCV infection -
 XX Claim 4; Fig 17; 308pp; English.

CC The present invention relates to human immunopolyptides, produced by a
 CC phage transfect cell library. The present sequence is one such
 CC immunopolyptide. The immunopolyptides have binding specificity for
 CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
 CC virus (HCV). E2 glycoprotein is believed to be responsible for target
 CC cell binding and contains neutralising epitopes, while NS3 is thought to
 CC be involved in the replication of HCV. The immunopolyptides are useful
 CC for diagnosing and treating a patient having or suspected to be having
 CC HCV infection.
 XX Sequence 32 AA;
 SQ Query Match 100.0%; Score 32; DB 23; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTUTISS 7
 DB 15 FTUTISS 21

RESULT 10
 ABP62688
 ID ABP62688 standard; Peptide; 32 AA.
 AC ABP62688;
 XX 10-OCT-2002 (first entry)
 XX Human immunopeptide to HCV E2 glycoprotein framework sequence #196.
 DE Virucide; human; immunopolyptide; immunopeptide; envelope glycoprotein;
 KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
 KW NS3 protein; viral infection.
 XX Homo sapiens.
 OS WO200259340-A1.
 XX 01-AUG-2002.
 XX 25-JAN-2002; 2002WO-US02303.
 XX 26-JAN-2001; 2001US-264451P.
 XX (SCRI) SCRIPPS RES INST.
 XX Maruyama T, Jones IM, Burton DR, Fox RI;
 XX WPI; 2002-599801/64.
 XX New human immunopolyptide with binding specificity for certain
 PT envelope glycoproteins and nonstructural proteins of hepatitis C virus
 PT (HCV), for diagnosing or treating patients having or suspected of
 PT having HCV infection -
 XX Claim 4; Fig 17; 308pp; English.

CC The present invention relates to human immunopolyptides, produced by a
 CC phage transfect cell library. The present sequence is one such
 CC immunopolyptide. The immunopolyptides have binding specificity for
 CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
 CC virus (HCV). E2 glycoprotein is believed to be responsible for target
 CC cell binding and contains neutralising epitopes, while NS3 is thought to
 CC be involved in the replication of HCV. The immunopolyptides are useful
 CC for diagnosing and treating a patient having or suspected to be having
 CC HCV infection.
 XX Sequence 32 AA;
 SQ Query Match 100.0%; Score 32; DB 23; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTUTISS 7
 DB 15 FTUTISS 21

RESULT 10
 ABP62688
 ID ABP62688 standard; Peptide; 32 AA.
 AC ABP62688;
 XX 10-OCT-2002 (first entry)
 XX Human immunopeptide to HCV E2 glycoprotein framework sequence #196.
 DE Virucide; human; immunopolyptide; immunopeptide; envelope glycoprotein;
 KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
 KW NS3 protein; viral infection.
 XX Homo sapiens.
 OS WO200259340-A1.
 XX 01-AUG-2002.
 XX 25-JAN-2002; 2002WO-US02303.
 XX 26-JAN-2001; 2001US-264451P.
 XX (SCRI) SCRIPPS RES INST.
 XX Maruyama T, Jones IM, Burton DR, Fox RI;
 XX WPI; 2002-599801/64.
 XX New human immunopolyptide with binding specificity for certain
 PT envelope glycoproteins and nonstructural proteins of hepatitis C virus
 PT (HCV), for diagnosing or treating patients having or suspected of
 PT having HCV infection -
 XX Claim 4; Fig 17; 308pp; English.

XX DE Human light chain immunoglobulin framework region 3 #1.
 XX XX
 KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IgBP;
 KW transgenic plant; immunoglobulin binding protein array;
 KW IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
 XX KW
 OS Homo sapiens.
 XX XX
 FN WO200193806-A1.
 XX XX
 PD 08-NOV-2001.
 XX XX
 PF 02-MAY-2001; 2001WO-US14349.
 XX XX
 PF 02-MAY-2000; 2000US-0563222.
 XX XX
 PR (EPIC-) EPICYTE PHARM INC.
 XX PA
 XX Hiatt AC, Hein MB;
 XX PI
 XX DR WPI; 2002-055482/07.
 XX DR
 XX
 PT Preparing immunoglobulin binding protein array in plant cells by
 PT transforming the cells with different polynucleotides encoding binding
 PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array
 XX PS
 XX Disclosure; Fig 1A; 129pp; English.
 XX CC
 CC The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IgBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IgBP that
 CC binds to a ligand, and transformed plant cells are selected, and
 CC preparing an IgBP array in plant cells. At least one peptide sequence has
 CC at least 75% sequence identity to a framework region (FR) of a native
 CC IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule.
 CC The method is useful for preparing an immunoglobulin binding protein
 CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic
 CC cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)
 CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The
 CC CHBP is useful for discovery of e.g. screening assays of IgBPs having
 CC desired characteristics. The present sequence is a mammalian
 CC immunoglobulin derived peptide that may be incorporated into an IgBP of
 CC the invention.
 XX SQ Sequence 32 AA;
 Query Match 100.0%; Score 32; DB 23; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 1 FTLTSS 7
 |||||
 15 FTLTSS 21

RESULT 14
 AAU70408
 ID AAU70408 standard; Peptide; 32 AA.
 AC AAU70408;
 AC XX
 DT 14-FEB-2002 (first entry)
 DT XX
 DE Human light chain immunoglobulin framework region 3 #4.
 DE XX
 KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IgBP;
 KW transgenic plant; immunoglobulin binding protein array;

KW IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
 XX XX
 OS Homo sapiens.
 XX XX
 FN WO200193806-A1.
 XX XX
 PD 08-NOV-2001.
 XX XX
 PF 02-MAY-2001; 2001WO-US14349.
 XX XX
 PF 02-MAY-2000; 2000US-0563222.
 XX XX
 PR (EPIC-) EPICYTE PHARM INC.
 XX PA
 XX Hiatt AC, Hein MB;
 XX PI
 XX DR WPI; 2002-055482/07.
 XX DR
 XX
 PT Preparing immunoglobulin binding protein array in plant cells by
 PT transforming the cells with different polynucleotides encoding binding
 PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array
 XX PS
 XX Disclosure; Fig 1A; 129pp; English.
 XX CC
 CC The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IgBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IgBP that
 CC binds to a ligand, and transformed plant cells are selected, and
 CC preparing an IgBP array in plant cells. At least one peptide sequence has
 CC at least 75% sequence identity to a framework region (FR) of a native
 CC IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule.
 CC The method is useful for preparing an immunoglobulin binding protein
 CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic
 CC cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)
 CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The
 CC CHBP is useful for discovery of e.g. screening assays of IgBPs having
 CC desired characteristics. The present sequence is a mammalian
 CC immunoglobulin derived peptide that may be incorporated into an IgBP of
 CC the invention.
 XX SQ Sequence 32 AA;
 Query Match 100.0%; Score 32; DB 23; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 FTLTSS 7
 |||||
 15 FTLTSS 21

RESULT 15
 AAU70436
 ID AAU70436 standard; Peptide; 32 AA.
 AC AAU70436;
 AC XX
 DT 14-FEB-2002 (first entry)
 DT XX
 DE Mouse light chain immunoglobulin framework region 3 #1.
 DE XX
 KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IgBP;
 KW transgenic plant; immunoglobulin binding protein array;
 KW IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
 XX OS
 OS Mus musculus.
 XX XX
 FN WO200193806-A1.

PD 08-NOV-2001.
XX
XX PF 02-MAY-2001; 2001WO-US14349.
XX
XX PR 02-MAY-2000; 2000US-0563222.
XX
XX PA (EPIC-) EPICYTE PHARM INC.
XX
XX PI Hiatt AC, Hain MS;
XX
XX DR WPI; 2002-065462/07.
XX
XX PT Preparing immunoglobulin binding protein array on plant cells by
XX transforming the cells with different polynucleotides encoding binding
XX protein polypeptides specific to ligand, selecting plant cells for
XX preparing array -
XX
XX PS Disclosure; Fig 1A; 123pp; English.
XX
XX CC The invention relates to transforming a population of cells (e.g. plant
XX cells), comprising using a library of two different polynucleotides
XX encoding different immunoglobulin binding protein (IgBP) polypeptides
XX that specifically bind to a ligand or form one or more disulphide bonds
XX with polypeptides in transfected cells, to generate an IgBP that
XX binds to a ligand, and transformed plant cells are selected, and
XX preparing an IgBP array in plant cells. At least one peptide sequence has
XX at least 75% sequence identity to a framework region (FR) of a native
XX IgM, IgG, IgA, IgD, IgE, IgF, kappa or lambda immunoglobulin molecule.
XX The method is useful for preparing an immunoglobulin binding protein
XX array, preferably heavy chain binding protein (CHBP) array in eukaryotic
XX cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)
XX or other eukaryotic cells (e.g. insect cells or mammalian cells). The
XX CHBP is useful for discovery of e.g. screening assays of IgBPs having
XX desired characteristics. The present sequence is a mammalian having
XX immunoglobulin derived peptide that may be incorporated into an IgBP of
XX the invention.
XX
XX SQ Sequence 32 AA;

Query Match 100.0%; Score 32; DB 23; Length 32;
Best Local Similarity 100.0%; Pred. NC. 4.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FTLTSS 7
Db 15 FTLTSS 21

Search completed: October 4, 2003, 12:21:57
Job time : 62.3333 secs


```
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-95

Query Match: 100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
Db 15 FTLTSS 21

RESULT 3
US-09-828-708-96
; Sequence 96 Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-96

Query Match: 100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
Db 15 FTLTSS 21

RESULT 4
US-09-828-708-98
; Sequence 98 Application US/39826708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-828-708-98

Query Match: 100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
Db 15 FTLTSS 21

RESULT 5
US-09-949-559-91
; Sequence 91 Application US/09949559
; Patent No. US20020151682A1
; GENERAL INFORMATION:
; APPLICANT: Achwal, Diljeet Singh
; APPLICANT: Brown, Derek Thomas
; APPLICANT: Weir, Andrew Neil Charles
; APPLICANT: Popplewell, Andrew George
; APPLICANT: Chapman, Andrew Paul
; APPLICANT: King, David John
; TITLE OF INVENTION: Biological Products
; FILE REFERENCE: Carp-0095
; CURRENT APPLICATION NUMBER: US/09/949,559
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 00138-0.7GB
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 03/875,221
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human group 1 consensus framework 13
US-09-949-559-91

Query Match: 100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
Db 15 FTLTSS 21

RESULT 6
US-09-874-141-15
; Sequence 15 Application US/09874141
; Publication No. US2003001278-A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL
; APPLICANT: PAN, LI-ZHEN
; APPLICANT: HANNA, NABIL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: KLOETZER, WILLIAM S.
; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP19, COMPOSITIONS
; FILE REFERENCE: 037003-0280632
; CURRENT APPLICATION NUMBER: US/09/874,141
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,584
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-874-141-15

Query Match 100.0%; Score 32; DB 11; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
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Db 15 FTLTSS 21

RESULT 7

US-09-875-221A-91
; Sequence 91, Application US/09875221A
; Publication No. US20030026805A1
; GENERAL INFORMATION:
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Brown, Derek Thomas
; APPLICANT: Weir, Andrew Neil Charles
; APPLICANT: Popplewell, Andrew George
; APPLICANT: Chapman, Andrew Paul
; APPLICANT: King, David John
; TITLE OF INVENTION: Biological Products
; FILE REFERENCE: Catp-0089
; CURRENT APPLICATION NUMBER: US/09/875,221A
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: GB0013810.7
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 91
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human group 1 consensus framework L3
US-09-875-221A-92

Query Match 100.0%; Score 32; DB 11; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
|||||
Db 15 FTLTSS 21

RESULT 8

US-09-563-222-76
; Sequence 76, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-76

Query Match 100.0%; Score 32; DB 11; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
|||||

Db 15 FTLTSS 21

RESULT 9

US-09-563-222-88
; Sequence 88, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-88

Query Match 100.0%; Score 32; DB 11; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
|||||
Db 15 FTLTSS 21

RESULT 10

US-09-563-222-116
; Sequence 116, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-116

Query Match 100.0%; Score 32; DB 11; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
|||||
Db 15 FTLTSS 21

RESULT 11

US-10-160-506-15
; Sequence 15, Application US/10160506
; Publication No. US20030161832A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
; TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
; TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
; FILE REFERENCE: 10448-162001
; CURRENT APPLICATION NUMBER: US/10/160,506
; CURRENT FILING DATE: 2002-05-30

PRIOR APPLICATION NUMBER: 60/324,100
PRIOR FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/362,612
PRIOR FILING DATE: 2002-03-08
NUMBER OF SEQ ID NOS: 128
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 32
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: deimmunized light chain J591
US-10-160-506-15

Query Match 100.0%; Score 32; DB 12; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
Db 15 FTLTSS 21

RESULT 12
US-10-387-645-5
Sequence 5, Application US/10387645
Publication No. US20030175845A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: KALBAG, Suresh M.
APPLICANT: KARUNATILAKE, Chulani
TITLE OF INVENTION: USE OF SPLITOLYSIS IN HIGH PERFORMANCE
TITLE OF INVENTION: PEPTIDE MAPPING
FILE REFERENCE: 39766-0102A
CURRENT APPLICATION NUMBER: US/10/387,645
CURRENT FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 60/364,992
PRIOR FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 36
TYPE: PRT
ORGANISM: homo sapiens
US-10-387-645-5

Query Match 100.0%; Score 32; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
Db 5 FTLTSS 11

RESULT 13
US-09-874-141-16
Sequence 16, Application US/09874141
Publication No. US20030012781A1
GENERAL INFORMATION:
APPLICANT: ANDERSON, DARRELL
APPLICANT: PAN, LI-ZHEN
APPLICANT: HANNA, NABIL
APPLICANT: RASTETTER, WILLIAM H.
APPLICANT: KLOETZER, WILLIAM S.
TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GR39, COMPOSITIONS
TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0280632
CURRENT APPLICATION NUMBER: US/09/874,141
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/209,584
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 53

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-09-874-141-16

Query Match 100.0%; Score 32; DB 11; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
Db 15 FTLTSS 21

RESULT 14
US-09-874-141-18
Sequence 18, Application US/09874141
Publication No. US20030012781A1
GENERAL INFORMATION:
APPLICANT: ANDERSON, DARRELL
APPLICANT: PAN, LI-ZHEN
APPLICANT: HANNA, NABIL
APPLICANT: RASTETTER, WILLIAM H.
APPLICANT: KLOETZER, WILLIAM S.
TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GR39, COMPOSITIONS
TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0280632
CURRENT APPLICATION NUMBER: US/09/874,141
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/209,584
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 42
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: humanized VL#1 peptide
US-09-874-141-18

Query Match 100.0%; Score 32; DB 11; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
Db 15 FTLTSS 21

RESULT 15
US-09-874-141-22
Sequence 22, Application US/09874141
Publication No. US20030012781A1
GENERAL INFORMATION:
APPLICANT: ANDERSON, DARRELL
APPLICANT: PAN, LI-ZHEN
APPLICANT: HANNA, NABIL
APPLICANT: RASTETTER, WILLIAM H.
APPLICANT: KLOETZER, WILLIAM S.
TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GR39, COMPOSITIONS
TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0280632
CURRENT APPLICATION NUMBER: US/09/874,141
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/209,584
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22


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, LENGTH: 42
, TYPE: PRT
, ORGANISM: Homo sapiens
US-09-874-141-22
Query Match      100.0%; Score 32; DB 11; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY      1 FTLTISS 7
Db      15 FTLTISS 21
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Search completed: October 4, 2003, 12:42:33
Job time : 36.3333 secs

GenCore version 5.1.6
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OX protein - protein: search, using sw model

Run on: October 4, 2003, 12:18:51 : Search time 17.6667 Seconds
(without alignments)
16.765 Million cell updates/sec

Title: US-09-712-819C-1

Perfect score: 32

Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 326717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	25	5	PCT-US91-02942-26
2	32	100.0	25	5	PCT-US91-02942-32
3	32	100.0	32	2	US-08-470-133-13
4	32	100.0	32	3	US-08-569-147-40
5	32	100.0	32	4	US-09-347-051-13
6	32	100.0	32	4	US-09-425-638A-92
7	32	100.0	32	4	US-09-425-638A-94
8	32	100.0	32	4	US-09-543-004-92
9	32	100.0	32	4	US-09-543-004-94
10	32	100.0	50	5	PCT-US91-02942-8
11	32	100.0	50	5	PCT-US91-02942-9
12	32	100.0	64	2	US-08-765-1793-10
13	32	100.0	64	2	US-08-765-1793-14
14	32	100.0	70	3	US-08-554-840-9
15	32	100.0	70	4	US-08-925-333-9
16	32	100.0	70	4	US-09-332-595-9
17	32	100.0	76	3	US-08-851-362D-21
18	32	100.0	80	3	US-08-554-840-10
19	32	100.0	80	3	US-08-554-840-12
20	32	100.0	80	3	US-08-554-840-13
21	32	100.0	80	3	US-08-554-840-15
22	32	100.0	80	4	US-08-925-333-10
23	32	100.0	80	4	US-08-925-333-12
24	32	100.0	80	4	US-08-925-333-13
25	32	100.0	80	4	US-08-925-333-15
26	32	100.0	80	4	US-09-332-595-10
27	32	100.0	80	4	US-09-332-595-12

Sequence 13, Appl
Sequence 15, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 19, Appl
Sequence 33, Appl
Sequence 16, Appl
Sequence 30, Appl
Sequence 33, Appl
Sequence 6, Appl
Sequence 3, Appl
Sequence 6, Appl
Sequence 10, Appl
Sequence 2, Appl
Sequence 42, Appl
Sequence 106, App
Sequence 106, App

ALIGNMENTS

RESULT 1
PCT-US91-02942-26
Sequence 26, Application PC/TUS9102942
GENERAL INFORMATION:
APPLICANT: ROTHLEIN, ROBERT
APPLICANT: ADAIR, JOHN R
TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Ave. NW Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02942
FILING DATE: 199.0429
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9009549.8
FILING DATE: 27-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: FOX, SAM L
REGISTRATION NUMBER: 30.353
REFERENCE/DOCKET NUMBER: 1011.0566600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PC-US91-02942-26

Query Match 100.0% Score 32: DB 5; Length 25;
Best Local Similarity 100.0%; Pred.No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7

Db 8 FTLTSS 14

RESULT 2
PCT-US91-02942-42
; Sequence 42, Application: PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: KOTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: AHWAL, DILBERT S
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steins, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 1991-04-29
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM J.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011-0586602
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 813-8716
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US91-02942-42

Query Match 100.0%; Score 32; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
DB 9 FTLTSS 14

RESULT 3
US-08-470-139-13
; Sequence 13, Application US/08470139
; Patent No. 5985866
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,139
; FILING DATE: 06 JUNE-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: TRUJILLO, DOREEN YATKO

; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0044
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-470-139-13

Query Match 100.0%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
DB 15 FTLTSS 21

RESULT 4
US-09-569-147-40
; Sequence 40, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6180377ris, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPC)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: pept:de
US-08-569-147-40

Query Match 100.0%; Score 32; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
DB 15 FTLTSS 21

RESULT 5
US-09-347-061-13
; Sequence 13, Application US/09347061

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; Patent No. 6316227
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Mark
; APPLICANT: Atwal, Diljeet Singh
; APPLICANT: Entage, John Spencer
; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
; FILE REFERENCE: CARP-0071
; CURRENT APPLICATION NUMBER: US/09/547,061
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Consensus
US-09-347-061-13

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : FTLTSS 7
Db 15 FTLTSS 21

RESULT 6
US-09-425-638A-92
; Sequence 92, Application US/09425638A
; Patent No. 6342587
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 563C
; CURRENT APPLICATION NUMBER: US/09/425,638A
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 92
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-425-638A-92

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : FTLTSS 7
Db 15 FTLTSS 21

RESULT 7
US-09-425-638A-94
; Sequence 94, Application US/09425638A
; Patent No. 6342587
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 563C
; CURRENT APPLICATION NUMBER: US/09/425,638A
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 94
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-425-638A-94

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : FTLTSS 7
Db 15 FTLTSS 21

RESULT 8
US-09-543-004-92
; Sequence 92, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 92
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-92

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : FTLTSS 7
Db 15 FTLTSS 21

RESULT 9
US-09-543-004-94
; Sequence 94, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 94
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-94

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : FTLTSS 7
Db 15 FTLTSS 21

RESULT 10
US-09-543-004-94
; Sequence 94, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630
; CURRENT APPLICATION NUMBER: US/09/425,638A
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 94
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-94

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : FTLTSS 7
Db 15 FTLTSS 21
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PCT-US91-02942-8
; Sequence 8, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAJE, JOHN R
; APPLICANT: ATHWAL, DILJEET S
; TITLE OF INVENTION: HUMANIZED COR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 456-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US91-02942-8
Query Match 100.0%; Score 32; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 FTLTSS 7
Db 26 FTLTSS 32
RESULT 11
PCT-US91-02942-9
; Sequence 9, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAJE, JOHN R
; APPLICANT: ATHWAL, DILJEET S
; TITLE OF INVENTION: HUMANIZED COR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 456-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US91-02942-9
Query Match 100.0%; Score 32; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 FTLTSS 7
Db 26 FTLTSS 32
RESULT 12
PCT-US91-02942-10
; Sequence 10, Application US/08765179B
; Patent No. 5854027
; GENERAL INFORMATION:
; APPLICANT: STEIPE, Boris
; APPLICANT: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
; TITLE OF INVENTION: OF ANTIBODIES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Cram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,179B
; FILING DATE: 14-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/02626
; FILING DATE: 06-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 25 115.7
; FILING DATE: 15-JUL-1994
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-765-179B-10
Query Match 100.0%; Score 32; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 6.1;

PCT-US91-02942-9
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 456-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US91-02942-9
Query Match 100.0%; Score 32; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 FTLTSS 7
Db 26 FTLTSS 32
RESULT 12
US-08-765-179B-10
; Sequence 10, Application US/08765179B
; Patent No. 5854027
; GENERAL INFORMATION:
; APPLICANT: STEIPE, Boris
; APPLICANT: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
; TITLE OF INVENTION: OF ANTIBODIES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Cram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,179B
; FILING DATE: 14-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/02626
; FILING DATE: 06-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 25 115.7
; FILING DATE: 15-JUL-1994
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-765-179B-10
Query Match 100.0%; Score 32; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 6.1;

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTSS 7
DB 40 FTLTSS 46
RESULT 13
US-08-765-179B-14
Sequence 9, Application US/08765179B
Patent No. 5854027
GENERAL INFORMATION:
APPLICANT: STEIFE, Boris
APPLICANT: STEINBACHER, Stefan
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
TITLE OF INVENTION: OF ANTIBODIES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,179B
FILING DATE: 14-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02626
FILING DATE: 06-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 25 115.7
FILING DATE: 15-JUL-1994
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: Protein
S-08-765-179B-14
Query Match 100.0%; Score 32; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1 FTLTSS 7
DB 40 FTLTSS 46
RESULT 14
S-08-554-840-9
Sequence 9, Application US/08554840
Patent No. 6001358
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabil
APPLICANT: PADLAN, Eduardo A.
APPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTSS 7
DB 53 FTLTSS 59
Query Match 100.0%; Score 32; DB 3; Length 70;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 15
US-08-925-339-9
Sequence 9, Application US/08925339
Patent No. 6440418
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabil
APPLICANT: PADLAN, Eduardo A.
APPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,339
FILING DATE: 07-NOV-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-554-840-9
Query Match 100.0%; Score 32; DB 3; Length 70;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTSS 7
DB 53 FTLTSS 59
Query Match 100.0%; Score 32; DB 3; Length 70;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 15
US-08-925-339-9
Sequence 9, Application US/08925339
Patent No. 6440418
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabil
APPLICANT: PADLAN, Eduardo A.
APPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,339
FILING DATE: 07-NOV-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
```

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; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-925-339-9

Query Match      100.0%; Score 32; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      : FTUTISS 7
Db      53 FTUTISS 59

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Search completed: October 4, 2003, 12:27:21
 Job time : 18.6667 secs


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JT0521
IG kappa chain V-III region (CP1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 09-May-1997
C:Accession: J0521
R:Anker, R.; Conley, M.E.; Pollok, B.A.
J. Exp. Med. 169, 2109-2119, 1999
A:Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia
A:Reference number: JT051; PMID:89279157; PMID:2786547
A:Accession: JT0521
A:Molecule type: mRNA
A:Residues: 1-54 <ANK>
A:Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangements
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-49/Domain: V region <VRE>
F:50-54/Domain: J region <JRE>

Query Match      100.0%; Score 35; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TDFTLTI 7
      |||||
DB      21 TDFTLTI 27

RESULT 4
S21526
IG kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 23-Jul-1999
C:Accession: S34082; S21526
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; PMID:83170387; PMID:8436174
A:Accession: S34082
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <WR2>
A:Cross-references: EMBL:X66042; NID:G33328; PID:CA446841.1; PID:G33329
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match      100.0%; Score 35; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TDFTLTI 7
      |||||
DB      62 TDFTLTI 68

RESULT 5
S34102
IG kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999
C:Accession: S34102
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; PMID:93170387; PMID:8436174
A:Accession: S34102
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-78 <WAG>
A:Cross-references: EMBL:X67156
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match      100.0%; Score 35; DB 2; Length 78;

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Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TDFTLTI 7
      |||||
DB      60 TDFTLTI 66

RESULT 6
S24215
IG kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24215
R:Shimizu, T.; Iwasato, T.; Yamagishi, H.
J. Exp. Med. 173, 1065-1072, 1991
A:Title: Deletions of immunoglobulin C(kappa) region characterized by the circular exc
A:Reference number: S24214; PMID:9127618; PMID:1902500
A:Accession: S24215
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-79 <SHI>
A:Cross-references: EMBL:X58202; NID:G53718; PID:CA441178.1; PID:G930195
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match      100.0%; Score 35; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TDFTLTI 7
      |||||
DB      42 TDFTLTI 48

RESULT 7
PH1048
IG light chain V region (clone 165.49) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PH1048
R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A:Reference number: PH0371; PMID:92381444; PMID:1512540
A:Accession: PH1048
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-81 <TIL>
A:Experimental source: B cell, strain (NZB x NZW)F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match      100.0%; Score 35; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TDFTLTI 7
      |||||
DB      54 TDFTLTI 60

RESULT 8
S38560
IG light chain V region (ASMB1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38560
R:Monesier, M.; Losman, L.J.; Novick, K.E.; Atis, J.P.
submitted to the EMBL Data Library, September 1993
A:Description: Molecular analysis of mercury-induced anti-nuclear antibodies in H-2s
A:Reference number: S38559
A:Accession: S38560

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C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16826; S34101
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid f
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 35; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy 1 TDFTLTI 7
Db 69 TDFTLTI 75

RESULT 9
S34090
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34090
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34090
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-82 <WAG>
A:Cross-references: EMBL:X67174
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 35; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy 1 TDFTLTI 7
Db 60 TDFTLTI 66

RESULT 10
I30607
Ig kappa chain V-III region (Wei) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-May-1997
C:Accession: I30607
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjencia, M.L.; Fernandez, J.; Carson, D.; Seid
J. Immunol. 142, 3158-3163, 1989
A:Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A:Reference number: A30601; MUID:89215279; PMID:2496160
A:Accession: I30607
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-83 <GON>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 35; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy 1 TDFTLTI 7
Db 70 TDFTLTI 76

RESULT 11
S16826
Ig kappa chain V region - human (fragment)

```

```

C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16826; S34101
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid f
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 35; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy 1 TDFTLTI 7
Db 60 TDFTLTI 66

RESULT 12
S16834
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16834
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid f
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16834
A:Status: preliminary; translation: not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54832
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 35; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy 1 TDFTLTI 7
Db 60 TDFTLTI 66

RESULT 13
S16836
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16836
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid f
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16836

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Search completed: October 4, 2003, 12:26:21
Job time : 20.3333 secs

A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54874
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 35; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
|||
DB 60 TDFTLTI 66

RESULT 14

S34086
IG kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34086
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; XJID:93170307; PMID:8436174
A:Accession: S34086

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <WAG>
A:Cross-references: EMBL:X57169
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 35; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
|||
DB 62 TDFTLTI 68

RESULT 15

S16840
IG kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16840
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; XJID:91243737; PMID:1903756
A:Accession: S16840

A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54838
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 35; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
|||
DB 60 TDFTLTI 66

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OM protein - protein search, using sw model

October 4, 2003, 12:09:51 : Search time 10.6667 Seconds
(without alignments)
30.861 Million cell updates/sec

Title: US-09-712-819c-5

Perfect score: 35

Sequence: 1 TDFTLTI 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
2	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
3	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
4	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
5	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
6	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
7	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
8	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
9	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
10	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
11	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
12	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
13	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
14	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
15	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
16	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
17	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
18	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
19	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
20	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
21	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
22	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
23	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
24	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
25	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
26	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
27	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
28	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
29	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
30	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
31	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
32	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
33	35	100.0	100	1 KV3C_HUMAN	P01621 homo sapien

RESULT 1
KV3C_HUMAN
ID KV3C_HUMAN STANDARD; PRT; 100 AA.
AC P01621;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region NG9 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94093600; PubMed=6419127;
RA Bentley D.L.;
RT "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to a small family of germ-line V genes.";
RL Nature 107:77-80(1984).
CC -!- MISCELLANEOUS: THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.
DR PIR; A01994; K3HUNG.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig-MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SMC0406; IG_V.
DR PROSITE; PS00835; IG_LIKES.
KW Immunoglobulin V region; Signal; Hybridoma.
FT NON TER 1 1
FT SIGNAL 4
FT CHAIN 5 100 IG KAPPA CHAIN V-III REGION NG9.
FT DISULFID 27 93 BY SIMILARITY.
FT NON TER 100 100
SQ SEQUENCE 100 AA; 10729 MW; 5D9AF363C052632F CRC64;

Query Match 100.0%; Score 35; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TDFTLTI 7
Db 74 TDFTLTI 80
RESULT 2
KV3C_HUMAN
ID KV3C_HUMAN STANDARD; PRT; 107 AA.
AC P01685;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V region 4135.

OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RN SEQUENCE.
 RX MEDLINE=75133568; PubMed=1091650;
 RA Chen K.C.S., Kindt T.J., Krause R.M.;
 RA "Primary structure of the L chain from a rabbit homogeneous antibody
 RT to streptococcal carbohydrate. II. Sequence determination of peptides
 RT from tryptic and peptic digests."
 RT C. Biol. Chem. 253:3289-3296(1975).
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE B4-TYPE C REGION IS ALSO GIVEN.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO THE
 CC SPECIFIC CARBOHYDRATE OF GROUP C STREPTOCOCCI AND WAS ISOLATED
 CC FROM THE SERUM OF A SINGLE RABBIT.
 DR PIR: A01949; K4B41.
 DR HSP; P80362; IWT.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003066; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region.
 KW FRAMEWORK-1;
 FT DOMAIN 25 35
 FT DOMAIN 36 50
 FT DOMAIN 51 57
 FT DOMAIN 58 69
 FT DOMAIN 90 96
 FT DOMAIN 97 106
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA; 11182 MW; 8F94C5FE60B7222 CRC64;
 Query Match 100.0%; Score 35; DB 1; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TDFLTIT 7
 DB 70 TDFLTIT 75

RESULT 3

KVLD HUMAN STANDARD; PRT; 107 AA.
 AC P01556;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region CAR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE.
 RX MEDLINE=75075135; PubMed=4216454;
 RA Milstein C.P., Deverson E.V.;
 RA "Primary structure of kappa light chain from a human myeloma
 RT protein."
 RT Eur. J. Biochem. 49:377-381(1974).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR; A01964; K1HJ4R.
 DR HSP; P80362; IWT.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003066; Ig_MHC.

DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Gycoprotein.
 FT CARBOHYD 28 N-LINKED (GLCNAC...)
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA; 11703 MW; E1BF0CF9844C3346 CRC64;
 Query Match 100.0%; Score 35; DB 1; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TDFLTIT 7
 DB 69 TDFLTIT 75

RESULT 4
 KV06 RABIT STANDARD; PRT; 108 AA.
 AC P01687;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V region BS-5.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RN SEQUENCE.
 RX MEDLINE=75127348; PubMed=4156171;
 RA Jaton J.-C.;
 RA "Comparison of the amino acid sequences of the variable regions of
 RT light chains derived from two homogeneous rabbit anti-pneumococcal
 RT antibodies."
 RJ Biochem. J. 141:15-25(1974).
 RN [2]
 RP AMIDES AT POSITIONS 37 AND 69.
 RA Jaton J.-C.;
 RA Submitted (JUN-1975) to the PIR data bank.
 CC -1- MISCELLANEOUS: THIS CHAIN DIFFERS FROM THE KAPPA CHAIN FROM RABBIT
 CC BS-1, ALSO OBTAINED FROM ANTI-BODY TO TYPE III PNEUMOCOCCI, AT 8
 CC POSITIONS IN THE V REGION.
 DR PIR; A90274; KVRB5.
 DR HSP; P80362; IWT.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003066; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT DISULFID 80 108
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11281 MW; CFB6D10BB7A5FCE CRC64;
 Query Match 100.0%; Score 35; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TDFLTIT 7
 DB 69 TDFLTIT 75

CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.

DR PIR: A01868; KIHUHU.

DR HSSP: P80382; IWT.

DR GO: GO:0005576; C:extracellular; NAS.

DR GO: GO:0003823; F:antigen binding activity; NAS.

DR GO: GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003006; IG_MHC.

DR InterPro: IPR003596; IG_v.

DR Pfam: PF00047; IG; 1.

DR SMART: SM00406; IGV; 1.

DR PROSITE: PS0835; IG LIKE; 1.

KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 35 49 FRAMEWORK-2.

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 57 88 FRAMEWORK-3.

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 98 107 FRAMEWORK-4.

FT DISULFID 23 88 BY SIMILARITY.

FT NON_TER 108 108

SQ SEQUENCE 108 AA; 11671 MW; 0803A61608D0618 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 108;

Best Local Similarity 100.0%; Pred. No. 0.42;

Matches 7; Conservative C; Mismatches 3; Indels 0; Gaps 0;

QY 1 TDFTLTI 7

DB 69 TDFTLTI 75

RESULT 7

KV:Q_HUMAN STANDARD; PRT; 108 AA.

AC P01609;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-1 region Scw.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=75059271; PubMed=4435756;

RA Eulitz M., Hilschmann N.;

RT "The primary structure of a human immunoglobulin L-chain of

RT kappa-type (Bence-Jones protein Scw.). II: The cyto-peptide

RT and the complete amino acid sequence.";

RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866 (1974).

CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)

CC -!- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.

DR PIR: A01875; KIHUSW.

DR HSSP: P01607; IREI.

DR GO: GO:0005576; C:extracellular; NAS.

DR GO: GO:0003823; F:antigen binding activity; NAS.

DR GO: GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003006; IG_MHC.

DR InterPro: IPR003596; IG_v.

DR Pfam: PF00047; IG; 1.

DR SMART: SM00406; IGV; 1.

DR PROSITE: PS0835; IG LIKE; 1.

KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 35 49 FRAMEWORK-2.

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 57 88 FRAMEWORK-3.

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 98 107 FRAMEWORK-4.

FT DISULFID 23 88 BY SIMILARITY.

FT NON_TER 108 108

SQ SEQUENCE 108 AA; 11661 MW; BD06E3500:7PIE51 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 108;

Best Local Similarity 100.0%; Pred. No. 0.42;

Matches 7; Conservative C; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7

DB 69 TDFTLTI 75

RESULT 6

KV:H_HUMAN STANDARD; PRT; 108 AA.

AC P01600;

DT 21-JUL-1986 (Rel. 01, Created);

DT 21-JUL-1986 (Rel. 01, Last sequence update);

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-1 region Hau.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=71032830; PubMed=4097974;

RA Watanabe S., Hilschmann N.;

RT "The primary structure of a monoclonal kappa-type immunoglobulin L-

RT chain of subgroup 2 (Bence-Jones Protein Hau): subdivision within

RT subgroups.";

RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).

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FT DOMAIN 57 88 FRAMEWORK-3
FT DOMAIN 89 37 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 98 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11764 MW; 32CECDEF9644414 CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 1; Length 108;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
DB 69 TDFTLTI 75

RESULT 8
KV5P MOUSE
ID ID KV5P MOUSE STANDARD; PRT; 108 AA.
AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V regions (Anti-arsenate antibodies).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN 1
RP SEQUENCE.
RX MEDLINE=79195288; PubMed=109517;
RA Vrana M., Rudikoff S., Potter M.;
RT "The structural basis of a haptene-inhibitable kappa-chain idiotype.";
RL J. Immunol. 122:1905-1910(1979).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR PIR: A92808; KWS61.
DR HSSP: P80362; IWTL.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 98 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11809 MW; FAE4CA36076F2AFE CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 1; Length 108;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
DB 69 TDFTLTI 75

RESULT 10
KV5R MOUSE
ID ID KV5R MOUSE STANDARD; PRT; 108 AA.
AC P01651;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region EPC 109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN 1
RP SEQUENCE.
RX MEDLINE=79195288; PubMed=109517;
RA Vrana M., Rudikoff S., Potter M.;
RT "The structural basis of a haptene-inhibitable kappa-chain idiotype.";
RL J. Immunol. 122:1905-1910(1979).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR PIR: B92808; KWS09.
DR HSSP: P01607; IREI.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR
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FT DOMAIN 57 88 FRAMEWORK-3
FT DOMAIN 89 37 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 98 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11764 MW; 32CECDEF9644414 CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 1; Length 108;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
DB 69 TDFTLTI 75

RESULT 9
KV5P MOUSE
ID ID KV5P MOUSE STANDARD; PRT; 108 AA.
AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V regions (Anti-arsenate antibodies).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN 1
RP SEQUENCE.
RX MEDLINE=79195288; PubMed=109517;
RA Vrana M., Rudikoff S., Potter M.;
RT "The structural basis of a haptene-inhibitable kappa-chain idiotype.";
RL J. Immunol. 122:1905-1910(1979).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR PIR: A92808; KWS61.
DR HSSP: P80362; IWTL.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 98 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11809 MW; FAE4CA36076F2AFE CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 1; Length 108;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
DB 69 TDFTLTI 75

RESULT 10
KV5R MOUSE
ID ID KV5R MOUSE STANDARD; PRT; 108 AA.
AC P01651;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region EPC 109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN 1
RP SEQUENCE.
RX MEDLINE=79195288; PubMed=109517;
RA Vrana M., Rudikoff S., Potter M.;
RT "The structural basis of a haptene-inhibitable kappa-chain idiotype.";
RL J. Immunol. 122:1905-1910(1979).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR PIR: B92808; KWS09.
DR HSSP: P01607; IREI.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR
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DR HSSP: P01607; IREL.
DR InterPro: IPR007113; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein.
DR DOMAIN 1 23 FRAMEWORK-1.
DR DOMAIN 24 35 COMPLEMENTARITY-DETERMINING-1.
DR DOMAIN 36 50 FRAMEWORK-2.
DR DOMAIN 51 57 COMPLEMENTARITY-DETERMINING-2.
DR DOMAIN 58 59 FRAMEWORK-3.
DR DOMAIN 90 92 COMPLEMENTARITY-DETERMINING-3.
DR DOMAIN 93 123 FRAMEWORK-4.
DR NON_TER 109 109
DR SEQUENCE 109 AA; 11947 MW; A25BFFBFFB5C84C6 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 TDFTLTI 7
DB 69 TDFTLTI 75

RESULT 15
KV3B HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-JI region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID:9606;
RN 1;
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794613;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Ka
RT group."
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01892; KGHUSI.
DR HSSP: P80362; IWTU.
DR GO: GO:0005576; Cxetracellular; NAS.
DR GO: GO:0003823; Antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; IGV; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7699C3BCD646FFB4 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 TDFTLTI 7
DB 70 TDFTLTI 76

Search completed: October 4, 2003, 12:22:36
Job time : 10.6667 secs
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db 69 TDFTLI 75

RESULT 2

Q96SA9	PRELIMINARY;	PRT;	1 C7 AA.
1D	Q96SA9;		
AC	Q96SA9;		
CD	Q1-DEC-2001 (TrEMBLRel. 19, Created)		
DT	Q1-DEC-2001 (TrEMBLRel. 19, Last sequence update);		
DT	Q1-DEC-2001 (TrEMBLRel. 23, Last annotation update);		
DT	Q1-MAR-2003 (TrEMBLRel. 23, Last annotation update);		
DE	Anti-streptococcal/anti-myosin immunoglobulin kappa light chain		
DE	variable region (fragment).		
OS	Homo sapiens (human).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OS	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
OX	NCBI TaxID:9606;		

RP SEQUENCE FROM N. A.

RA	MEDLINE=98375693; PubMed=9123075;
RX	
RA	Adderson E, Shikhar A R, Ward K E, Cunningham V W;
RT	"Molecular analysis of polyreactive monoclonal antibodies from
RT	rheumatic carditis: human anti-N-acetylglucosamine/anti--yosin
RT	antibody V region genes."
RL	J. Immunol. 151:2020-2031(1998);
CR	EMBL: U96396; AAB68785.1;
CR	InterPro: IPR03710; Ig-like.
CR	InterPro: IPR033006; Ig-MHC.
CR	InterPro: IPR033596; Ig_V.
CR	Pfam: PF00047; Ig_1.
CR	SMART: SM00456; GV1.
CR	PROSITE: PS52835; Ig-Like; 1.
FT	NON TER 137
FT	NON TER 137
SQ	SEQUENCE 107 AA; 1520 MW; 4BR43B3CA9577E16 CDD4;

Query Match

Best Local Similarity	100.0%	Pred. No.	3.6	Indels	0	Gaps	0
Matches	7	Conservative	0	Mismatches	0		
QY	:	TDFTLTI 7					
Db	69	TDFTLTI 75					
RESULT 3							
Q9ER29		PRELIMINARY;	PRT;	107 AA.			
ID	Q9ER29	PRELIMINARY;	PRT;	107 AA.			
AC	Q9ER29						
DT	01-MAR-2001	(TEMBLrel. 16, Created:					
DT	01-MAR-2001	(TEMBLrel. 16, Last sequence update)					
DT	01-MAR-2003	(TEMBLrel. 23, Last annotation update)					

J. Cell. Mol. Immunol. 12:21-26 (1996).

RN	[2]
RP	SEQUENCE FROM N.A.
RT	Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RA	"Construction and sequencing of the single-chain antibody gene of a
PT	human TNF-alpha specific monoclonal antibody";
RJ	Ti 4 Chun i Ta Hsueh Shuen Peo 19:373-376(1998).
RN	[3]
RP	SEQUENCE FROM N.A.
RT	Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RA	Submitted (MAY-2000) to the EMBL/GenBank/DBC databases.
RR	EMBL; AF262753; AAC23804.1 ; -
AC	O9UL77 PRELIMINARY; PRT; 168 AA.
DT	01-MAY-2000 (TEMBLrel_13, Created)
DI	01-MAY-2000 (TEMBLrel_13, Last sequence update)
DR	01-MAR-2003 (TEMBLrel_23, Last annotation update)
DE	Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

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OX NCBI_TaxID=9606;
NRN [1]_
RRP SEQUENCE FROM N.A.
RRP MEDLINE=98277139; PubMed=9614934;
RRP Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RRP Young D.C.;
RRP "Myosin-reactive autoantibodies in rheumatic carditis and normal
RRP fetus.";
RRL Clin. Immunol. Immunopathol. 87:184-192(1998).
RRL EMBL; AF035037; AAD56271.1; -.
RRL HSSP; P01607; IREI.
RDL InterPro; IPR007110; IG-like.
RDL InterPro; IPR003006; IG_MHC.
RDL InterPro; IPR003596; IG_V.
RDL Pfam; PF00047; IG; 1.
RDL SMART; SM00406; IGV; 1.
RDL PROSITE; PSS0835; IG_LIKE; 1.
RDL NON_TER 1
RDL NON_TER 1
RDL NON_TER 1
SQ SEQUENCE 108 AA; 11738 MW; C0668171C4D16F3 CRC64;

Query Match 100.0%; Score 35; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TDFTLT 7
Db 69 TDFTLT 75

RESULT 6
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
DE Homo sapiens (Human).
DE Clin. Immunol. Immunopathol. 87:184-192(1998).
DE EMBL; AF035035; AAD56271.1; -.
DE HSSP; P01607; IREI.
DE InterPro; IPR007110; IG-like.
DE InterPro; IPR003006; IG_MHC.
DE InterPro; IPR003596; IG_V.
DE Pfam; PF00047; IG; 1.
DE SMART; SM00406; IGV; 1.
DE PROSITE; PSS0835; IG_LIKE; 1.
DE NON_TER 1
DE NON_TER 1
SQ SEQUENCE 108 AA; 11767 MW; D55845F13724F4E2 CRC64;

Query Match 100.0%; Score 35; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLT 7
Db 69 TDFTLT 75

RESULT 7
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
DE Homo sapiens (Human).
DE Clin. Immunol. Immunopathol. 87:184-192(1998).
DE EMBL; AF035035; AAD56271.1; -.
DE HSSP; P01607; IREI.
DE InterPro; IPR007110; IG-like.
DE InterPro; IPR003006; IG_MHC.
DE InterPro; IPR003596; IG_V.
DE Pfam; PF00047; IG; 1.
DE SMART; SM00406; IGV; 1.
DE PROSITE; PSS0835; IG_LIKE; 1.
DE NON_TER 1
DE NON_TER 1
SQ SEQUENCE 108 AA; 11767 MW; D55845F13724F4E2 CRC64;

Query Match 100.0%; Score 35; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLT 7
Db 69 TDFTLT 75

RESULT 7
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```
Q8VIJ0 PRELIMINARY; PRT; 108 AA.
AC Q8VIJ0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti-DNA light chain (Fragment).
DE VK19.
DE Mus musculus (Mouse).
DE Clin. Immunol. Immunopathol. 87:184-192(1998).
DE EMBL; AF035037; AAD56271.1; -.
DE HSSP; P01607; IREI.
DE InterPro; IPR007110; IG-like.
DE InterPro; IPR003006; IG_MHC.
DE InterPro; IPR003596; IG_V.
DE Pfam; PF00047; IG; 1.
DE SMART; SM00406; IGV; 1.
DE PROSITE; PSS0835; IG_LIKE; 1.
DE NON_TER 1
DE NON_TER 1
SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBFBE CRC64;

Query Match 100.0%; Score 35; DB 11; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLT 7
Db 69 TDFTLT 75

RESULT 8
Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
DE Homo sapiens (Human).
DE Clin. Immunol. Immunopathol. 87:184-192(1998).
DE EMBL; AF035028; AAD56264.1; -.
DE HSSP; P80362; IWTL.
DE InterPro; IPR007110; IG-like.
DE InterPro; IPR003006; IG_MHC.
DE InterPro; IPR003596; IG_V.
DE Pfam; PF00047; IG; 1.
DE SMART; SM00406; IGV; 1.
DE PROSITE; PSS0835; IG_LIKE; 1.
DE NON_TER 1
DE NON_TER 1
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;
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RC STRAIN=MGAS8232 / Serotype V19;
RX MEDLINE=21927593; PubMed=11071103;
RA Smoot J.C., Barban K.F., Van Gompel J.C., Smoot L.M., Chaussee M.S.,
RA Sylva G.B., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.N., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RA "Genome sequence and comparative microarray analysis of serotype V19
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4669-4673(2002).
RL EMBL: AE010116; AAL38593.1; -.
DR InterPro: IPR000559; Pmlettyd_synch.
DR Pfam: PF01268; FTHFS.2; 1.
DR PROSITE: PS00722; FTHFS.2; 1.
DR Ligase: Complete proteome: Hypothetical protein.
SQ SEQUENCE 557 AA; 59054 MW; 7A7222A02BDSA04 CRC64;

Query Match 91.4%; Score 32; DB 16; Length 557;
Best Local Similarity 85.7%; Pred. No. 96;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7
Db 505 TDFTVTI 511

RESULT 13
Q8KSL8 PRELIMINARY; PRT; 557 AA.
AC Q8KSL8;
DT 01-OCT-2002 (TREMBLrel. 22, Created);
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update);
DI 01-MAR-2003 (TREMBLrel. 23, Last annotation update);
DE Putative formate-tetrahydrofolate ligase.
EN FHS.2 OR SPYM3 1776.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
CC Streptococcus.
CX NCBI_TaxID=198466;
DR [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=2233803; PubMed=1212206;
RA Beres S.B., Sylva G.B., Barban K.D., Loi B., Hoff J.S.,
RA Mamarella N.B., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.N., McCormick J.K., Leung D.Y.N.,
RA Schlievert P.M., Musser J.M.;
RA "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RL EMBL: AE014171; AAY60383.1; -.
DR InterPro: IPR000559; Pmlettyd_synch.
DR Pfam: PF01268; FTHFS.2; 1.
DR PROSITE: PS00722; FTHFS.2; 1.
DR Ligase: Complete proteome: Hypothetical protein.
SQ SEQUENCE 557 AA; 59051 MW; 029820CF95BB401A CRC64;

Query Match 91.4%; Score 32; DB 16; Length 557;
Best Local Similarity 85.7%; Pred. No. 96;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7
Db 505 TDFTVTI 511

RESULT 14
Q9JL74 PRELIMINARY; PRT; 99 AA.
AC Q9JL74;
DT 01-OCT-2000 (TREMBLrel. 15, Created);
DI 01-OCT-2000 (TREMBLrel. 15, Last sequence update);

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DI 01-MAR-2003 (TREMBLrel. 23, Last annotation update);
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RF SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=1092488;
RA Walker S., Liao L., Cunningham M.W., Diamond B.;
RA "Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RL with cardiac myosin";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL: AF206032; AAF69330.1; -.
DR HSP; P80362; IWTL.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 10939 MW; 3B25D0E78453324 CRC64;

Query Match 88.6%; Score 31; DB 11; Length 99;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7
Db 61 TDFTFI 67

RESULT 15
Q9JL83 PRELIMINARY; PRT; 108 AA.
AC Q9JL83;
DT 01-MAY-2000 (TREMBLrel. 13, Created);
DI 01-MAY-2000 (TREMBLrel. 13, Last sequence update);
DI 01-MAR-2003 (TREMBLrel. 23, Last annotation update);
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
CX NCBI_TaxID=9606;
DR [1]
RF SEQUENCE FROM N.A.
RC MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035031; AAD56267.1; -.
DR HSP; P80362; IWTL.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SMC0406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 88.6%; Score 31; DB 4; Length 108;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 TDETC 7
Db 69 TDETC 75

Search completed: October 4, 2003, 12:25:17
Job time : 52.6667 secs

GenCore version 5.1.6
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MM protein - protein search, using sw model

Run on: October 4, 2003, 12:05:26 : Search time 60.3333 seconds
(without alignments)
18.416 Million cells updated/svc

Title: US-09-712-819c-5

Perfect score: 35

Sequence: 1 TDF:LLI ?

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

searched: 1107863 seqs, 158726573 residues

total number of hits satisfying chosen parameters: 1107863

inimum DB seq length: 6

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database : A Geneseq 19Jun03.:

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	35	100.0	16	AA19874	Rheumatoid arthritis
2	35	100.0	16	AAU25389	Schizophrenia-Asso
3	35	100.0	16	AAU15733	Schizophrenia-Asso
4	35	100.0	16	ABG78872	Multiple sclerosis
5	35	100.0	22	ABP56813	Kappa light chain
6	35	100.0	29	ABP62758	Human immunoglobulin
7	35	100.0	32	AAAR87043	Human group 1 high
8	35	100.0	32	AAV52745	Humanised ATR-5
9	35	100.0	32	AA898286	Anti-A33 antigen 1

10	35	100.0	32	22	AA898288	Anti-A33 antigen 1
11	35	100.0	32	22	AA897666	A33 antigen bindin
12	35	100.0	32	22	AA897668	A33 antigen bindin
13	35	100.0	32	23	ABG98287	Human antibody 0.2
14	35	100.0	32	23	ABP62656	Human immunopeptid
15	35	100.0	32	23	ABP62657	Human immunopeptid
16	35	100.0	32	23	ABP62658	Human immunopeptid
17	35	100.0	32	23	ABP62659	Human immunopeptid
18	35	100.0	32	23	ABP62660	Human immunopeptid
19	35	100.0	32	23	ABP62661	Human immunopeptid
20	35	100.0	32	23	ABP62664	Human immunopeptid
21	35	100.0	32	23	ABP62666	Human immunopeptid
22	35	100.0	32	23	ABP62667	Human immunopeptid
23	35	100.0	32	23	ABP62668	Human immunopeptid
24	35	100.0	32	23	ABP62669	Human immunopeptid
25	35	100.0	32	23	ABP62670	Human immunopeptid
26	35	100.0	32	23	ABP62671	Human immunopeptid
27	35	100.0	32	23	ABP62675	Human immunopeptid
28	35	100.0	32	23	ABP62676	Human immunopeptid
29	35	100.0	32	23	ABP62677	Human immunopeptid
30	35	100.0	32	23	ABP62678	Human immunopeptid
31	35	100.0	32	23	ABP62680	Human immunopeptid
32	35	100.0	32	23	ABP62682	Human immunopeptid
33	35	100.0	32	23	ABP62683	Human immunopeptid
34	35	100.0	32	23	ABP62684	Human immunopeptid
35	35	100.0	32	23	ABP62685	Human immunopeptid
36	35	100.0	32	23	ABP62687	Human immunopeptid
37	35	100.0	32	23	ABP62688	Human immunopeptid
38	35	100.0	32	23	ABP62689	Human immunopeptid
39	35	100.0	32	23	ABP62690	Human immunopeptid
40	35	100.0	32	23	AAO17642	Human FAPalpha spe
41	35	100.0	32	23	AAO17650	Human FAPalpha spe
42	35	100.0	32	23	AAE19672	Human group 1 cons
43	35	100.0	32	23	AAE19673	Human tumour necro
44	35	100.0	32	23	AAU70396	Human light chain
45	35	100.0	32	23	AAU70494	Human light chain

ALIGNMENTS

RESULT 1
AA19874
ID AAY41874 standard; Peptide: 16 AA.
XX
AC AAY41874;
XX
DT 09-DEC-1999 (first entry)
XX
DE Rheumatoid arthritis diagnostic protein isoform peptide #25.
XX
KW Human: rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;
KW Rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;
KW Rheumatoid arthritis diagnostic protein isoform; screening;
KW expression reference protein isoform; prognosis.
XX
OS Homo sapiens.
XX
PK WC9947925-A2.
PK
PD 23-SEP-1999.
XX
PF 15-MAR-1999; 99WO-GB00763.
XX
PR 13-MAR-1999; 98GB-0005477.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Parekh RB, Patel TP, Townsend RR;
XX
DR WPI; 1999-571871/48.
XX
PT Diagnosis of human rheumatoid arthritis by two-dimensional

PT electrophoresis -

PS Disclosure, Page 18; 157pp; English.

XX A method has been developed for the diagnosis of human rheumatoid
XX arthritis (RA) using two-dimensional electrophoresis to generate a
XX two-dimensional array of features. The method can be used for screening,
XX diagnosis and prognosis of RA in a subject or for monitoring the effect
XX of an anti-RA drug or therapy administered to a subject. The method
XX comprises: (a) analysing a sample of serum or plasma and optionally
XX synovial fluid by two-dimensional electrophoresis, to generate a two-
XX dimensional array of features; (b) identifying at least one chosen
XX feature whose relative abundance correlates with the presence or absence
XX of RA; and (c) comparing the abundance of each chosen feature in the
XX sample with the abundance of that chosen feature in serum or plasma from
XX one or more persons without RA, where the relative abundance of the
XX chosen feature or features in the sample indicates the presence or
XX absence of RA in the subject. The method can also be used in clinical
XX studies for testing drugs for therapy of RA, for purification of RA-
XX diagnostic protein isoforms (SPIs), and for production of antibodies to
XX SPIs. The RA-diagnostic feature (RA-DF) proteins can be used to identify
XX compounds that promote or inhibit their activity, which are then used as
XX RA drugs. Nucleic acid encoding RADFs can be used in gene therapy
XX protocols. AA41844 to AA42100 represent SPI peptides, AA42101 to
XX AA42103 represent expression reference protein isoform peptides and
XX AA225066 to AA225068 represent degenerate probes for SPIs, which are all
XX used in the exemplification of the present invention.

XX Sequence 16 AA;

Query Match 100.0%; Score 35; DB 20; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7

DB 8 TDFTLTI 14

RESULT 2

AAU25389
ID AAU25389 standard; Peptide; 16 AA.

XX AAU25389;

XX 18-DEC-2001 (first entry)

XX Schizophrenia-Associated Protein Isoform (SPI) peptide #518.

XX Schizophrenia-associated protein isoform; SPI; SPI-238; SPI-240;
KW neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.

XX Homo sapiens.

XX WO200162785-A2.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-GB00792.

XX 24-FEB-2000; 2000GB-0004415.

XX 28-NOV-2000; 2000US-0750395.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMAC, Parekh RB, Rohlff C, Terrett JA, Tyson KL;

XX WPI; 2001-570624/54.

XX New schizophrenia associated protein isoforms and encoding nucleic acid
XX molecules, useful for treatment, diagnosis and prognosis of
XX schizophrenia and screening for potential drugs for treatment and new
XX drug targets.

XX Disclosure, Page 41; 149pp; English.

XX The sequence represents a schizophrenia-associated protein isoform (SPI).
XX These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
XX in cerebrospinal fluid, serum or plasma and are useful markers of
XX schizophrenia. The sequences can be used for treatment and diagnosis of
XX schizophrenia, screening, prognosis, monitoring the results of therapy,
XX identifying patients most likely to respond to a particular therapy and
XX identification of new targets for drug treatment. SPI DNA is useful as a
XX nucleic acid probe to detect the presence of nucleic acids or SPIs.

XX Sequence 16 AA;

Query Match 100.0%; Score 35; DB 22; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7

DB 8 TDFTLTI 14

RESULT 3

AAU15733
ID AAU15733 standard; Peptide; 16 AA.

XX AAU15733;

XX 24-OCT-2001 (first entry)

XX Schizophrenia-associated isoform peptide #618.

XX Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
XX neurological disorder; neuropathy.

XX Homo sapiens.

XX WO200163293-A2.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-GB00753.

XX 24-FEB-2000; 2000GB-0004415.

XX 28-NOV-2000; 2000US-0750395.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMAC, Parekh RB, Rohlff C;

XX WPI; 2001-502868/55.

XX Diagnosing and monitoring Schizophrenia by detecting the presence of
XX Schizophrenia Associated Features and Schizophrenia Associated Protein
XX Isoforms in samples of cerebrospinal fluid -

XX Claim 6; Page 41; 160pp; English.

XX The invention relates to methods and compositions for screening,
XX diagnosis and prognosis of Schizophrenia. The method involves detecting
XX the presence of Schizophrenia (SCH) Associated Features (SfS) and SCH
XX Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,
XX immunoassay or hybridisation assay, for diagnosing and monitoring SCH.
XX Studying the effectiveness of treatments and for identifying potential
XX therapeutic agents. The method is used for (1) screening or diagnosis of
XX SCH and the relative abundance of at least 1 chosen feature correlates
XX with the presence or absence of SCH; and (2) monitoring the effect of
XX therapy administered to a subject with SCH and the relative abundance of
XX at least 1 chosen feature which correlates with the severity of SCH.
XX The expression and activity of the SfS, SPIs and related molecules
XX (e.g. secondary messengers) are studied to diagnose SCH, monitor the
XX progress of the disorder and the effectiveness of treatment and as

CC targets to identify and produce potential therapeutic agents for the
CC treatment of SCH. The paucity of detectable neurologic defects
CC distinguishes neuropsychiatric disorders such as SCH from neurological
CC disorders, where manifestations of anatomical and biochemical changes
CC have been identified in many cases. Consequently the identification and
CC characterisation of cellular and/or molecular causative defects and
CC neuropathies are necessary for improved treatment of neuropsychiatric
CC disorders. AB015:14-AMU:5762 represent the amino acid sequences of
CC schizophrenia-associated isoforms used in the method of the invention.

XX Sequence 16 AA;

Query Match 100.0%; Score 35; DB 22; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 7; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

QY 1 TDFTLTI 7
|||
DB 8 TDFTLTI 14

RESULT 4

ABG78872
D ABG78872 standard; Peptide: 16 AA.

AC ABG78872;

DT 29-NOV-2002 (first entry)

DE Multiple sclerosis associated feature (MSF) tryptic digest peptide #360.

FX Multiple sclerosis; MS; Multiple sclerosis associated feature: MSF;
KW human; multiple sclerosis-associated protein isoform; MSPI;
WW antiinflammatory; neuroprotective.

CS Homo sapiens.

XX WO200259604-A2.

PD 01-AUG-2002.

PF 25-JAN-2002; 2002WO-GB03330.

PR 26-JAN-2002; 2001US-264404P.

PR 20-NOV-2001; 2001US-331647P.

PA (OXFC-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMAC, Perekh RB, Rohiff C;

PI WPI: 2002-599812/64.

PT Screening or diagnosing multiple sclerosis (MS), useful for e.g.
PT determining the stage or severity of MS comprises detecting the
PT presence of MS-associated features or protein isoforms by 2-dimensional
PT electrophoresis.

PS Disclosure: Page 36; 128pp; English.

XX This invention relates to a novel method for screening or diagnosing
XX multiple sclerosis (MS) in a subject to determine the stage or severity
XX of MS, to identify a subject at risk of developing MS or to monitor the
XX effect of a therapy administered. The method comprises analysing a
XX sample body fluid from the subject by two-dimensional electrophoresis
XX and detecting the presence of multiple sclerosis-associated features
XX (MSFs), or multiple sclerosis-associated protein isoforms (MSPIs).
XX The MSFs of the invention correspond to spots identified on a 2D gel
XX these proteins may have antiinflammatory or neuroprotective activity.
XX The methods of the invention and the compositions are useful for
XX clinical screening, diagnosis and treatment of MS, for monitoring the
XX effectiveness of MS treatment, for selecting participants in clinical
XX trials, for identifying patients most likely to respond to a particular
XX therapeutic treatment and for screening and developing drugs for

CC treatment of MS. Agents that modulate the expression or activity of an
CC MSPI are useful for treating MS, for preventing or delaying the onset or
CC development of MS, to prevent or delay the progression of MS, or to
CC ameliorate the symptoms MS. Nucleic acids comprising a sequence encoding
CC an MSPI, MSPI-related polypeptide, or their fragments are useful for
CC promoting MSPI function by gene therapy. The present sequence represents
CC a human multiple sclerosis associated feature tryptic digest
CC peptide of the invention.

XX Sequence 16 AA;

Query Match 100.0%; Score 35; DB 22; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 7; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

QY 1 TDFTLTI 7
|||
DB 8 TDFTLTI 14

RESULT 5

ABP56813

ID ABP56813 standard; Protein: 22 AA.

AC ABP56813;

DT 01-APR-2003 (first entry)

DE Kappa light chain A27:JH1 amino acid sequence #3.

FX Focused library; genetic package; antibody; kappa light chain; CDR;
KW lambda light chain; heavy chain; complementary determining region;
KW diversity.

CS Homo sapiens.

XX Synthetic.

XX WO200261071-A2.

PD 08-AUG-2002.

PF 18-DEC-2001; 2001WO-US50297.

PR 18-DEC-2000; 2000US-256380P.

PA (LACN/) LADNER R C.

PI Ladner RC;

PI WPI: 2003-067343/06.

PT Focused library of vectors or genetic packages for displaying or
PT expressing diversity of an antibody family, comprise variegated DNA
PT sequences encoding heavy, kappa or lambda light chain complementary
PT determining regions.

PS Disclosure: Page 69-69; 92pp; English.

XX The present invention describes a focused library of vectors or genetic
XX packages that display, display and express, or comprise a member of a
XX diverse family of human antibody related peptides, polypeptides and
XX proteins and collectively display, display or express, or comprise a
XX portion of the diversity of the antibody family, the vectors or genetic
XX packages being characterised by variegated DNA sequences that encode a
XX heavy chain, kappa or lambda light chain complementary determining region
XX 1 (CDR1), CDR2 or CDR3. The focused library of vectors or genetic
XX packages of the present invention are useful for displaying, or
XX displaying and expressing the focused diversity of the family. The
XX present invention, as compared to prior art, is less time consuming,
XX more efficient and less cumbersome in the construction of libraries of
XX vectors and genetic packages using diverse but focused populations of
XX DNA sequences. ABP5671 to ABP56816 and ABP22680 to ABP22747 represent
XX sequences used in the exemplification of the present invention.

XX 02-APR-1999; 99WO-JP01768.
 XX 03-APR-1998; 99JP-0051850.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Sato K, Adachi H, Yabuta H;
 XX WPI; 1999-620204/53.
 XX Humanised antibody recognizing human tissue factor, used for treatment
 XX of disseminated intravascular coagulation -
 XX Claim 17; Page 270; 291pp; Japanese.
 XX The present invention describes chimeric antibody (Ab) heavy (H) chains
 XX containing the variable region of the H chain of a mouse monoclonal Ab
 XX recognising human tissue factor (hTF) and the constant region of the H
 XX chain of a human Ab. The variable region is one of six specified
 XX sequences (which are the H chain variable regions from mouse monoclonal
 XX Ab's ATR-2.3.4.5,7 or 9). Also described are chimeric Ab light (L)
 XX chains containing the variable region of the L chain of a mouse
 XX monoclonal Ab recognising human tissue factor (hTF) and the constant
 XX region of the L chain of a human Ab, the variable region being one of six
 XX specified sequences (which are the L chain variable regions from mouse
 XX monoclonal Ab's ATR-2.3.4.5,7 or 8). The chimeric Ab's can be used for
 XX the treatment and prevention of thrombotic disease, especially of
 XX disseminated intravascular coagulation (DIC). The humanised antibody has
 XX the high hTF binding activity of the mouse monoclonal antibody but
 XX greatly reduced immunogenicity. AA233001 to AA233091 and Y527007 to
 XX AA52267 represent sequences used in the exemplification of the present
 XX invention.

XX Sequence 32 AA;

Query Match 100.0%; Score 35; DB 20; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 TDFTLTIT 7
 |||||
 Db 13 TDFTLTIT 19

RESULT 9

AA98286
 ID AAB98286 standard; Peptide; 32 AA.
 XX AAB98286;
 AC AAB98286;
 DT 20-AUG-2001 (first entry)
 XX Anti-A33 antigen immunoglobulin VL FR3 SEQ ID NO:92.
 XX Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
 XX immunoglobulin; complementarity determining region; CDR; cancer;
 XX cytotstatic; anticancer; colon cancer; stomach cancer.
 XX Homo sapiens.

WO200130393-A2.

03-MAY-2001.

20-OCT-2000; 2000WO-US29289.

22-OCT-1999; 99US-0425638.

04-APR-2000; 2000US-0543004.

(LUDW-) LUDWIG INST CANCER RES.

(SLOK) SLOAN KETTERING INST CANCER RES.

(SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C, Ritter G, Welt S, Old LJ;
 XX WPI; 2001-328613/34.
 XX Treating cancers, particularly of stomach and colon, that express A33
 XX antigen by administering conjugate of anticancer agent with specific
 XX immunoglobulin product -
 XX Claim 16; Page 40; 85pp; English.
 XX The present invention describes a method for treating cancers that
 XX express the A33 antigen. The method comprises administering an
 XX anti-cancer agent (i) conjugated to an immunoglobulin product (ii) that
 XX binds specifically to A33 and contains one or more of 13 specified
 XX complementarity determining regions (CDRs), given in AAB98286 to
 XX AAB98274. (i) has cytostatic activity. The method can be used for
 XX treating colon and stomach cancers. (ii), or the nucleic acid encoding
 XX it, can be used directly, in unconjugated form, for immunotherapy of
 XX cancer, and, when labeled, for detection or diagnosis of diseases
 XX associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
 XX AAB98321 represent sequences used in the exemplification of the
 XX present invention.

XX Sequence 32 AA;

Query Match 100.0%; Score 35; DB 22; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTIT 7
 |||||
 Db 13 TDFTLTIT 19

RESULT 10

AA98286
 ID AAB98286 standard; Peptide; 32 AA.
 XX AAB98286;
 AC AAB98286;
 DT 20-AUG-2001 (first entry)
 XX Anti-A33 antigen immunoglobulin VL FR3 SEQ ID NO:94.
 XX Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
 XX immunoglobulin; complementarity determining region; CDR; cancer;
 XX cytotstatic; anticancer; colon cancer; stomach cancer.
 XX Homo sapiens.

WO200130393-A2.

03-MAY-2001.

20-OCT-2000; 2000WO-US29289.

22-OCT-1999; 99US-0425638.

04-APR-2000; 2000US-0543004.

(LUDW-) LUDWIG INST CANCER RES.

(SLOK) SLOAN KETTERING INST CANCER RES.

(SCRI) SCRIPPS RES INST.

Barbas CF, Rader C, Ritter G, Welt S, Old LJ;
 WPI; 2001-328613/34.

Treating cancers, particularly of stomach and colon, that express A33
 antigen by administering conjugate of anticancer agent with specific
 immunoglobulin product -

Claim 16; Page 40; 85pp; English.

XX
 CC The present invention describes a method for treating cancers that
 CC express the A33 antigen. The method comprises administering an
 CC anticancer agent (I), conjugated to an immunoglobulin product (II) that
 CC binds specifically to A33 and contains one or more of 13 specified
 CC complementarity determining regions (CDRs), given in AAB98262 to
 CC AAB98274. (I) has cytostatic activity. The method can be used for
 CC treating colon and stomach cancers. (II), or the nucleic acid encoding
 CC it, can be used directly, in unconjugated form, for immunotherapy of
 CC cancer, and, when labeled, for detection or diagnosis of diseases
 CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
 CC AAB98321 represent sequences used in the exemplification of the
 CC present invention.
 CC
 XX SQ Sequence 32 AA;
 CC
 CC Query Match 100.0%; Score 35; DB 22; Length 32;
 CC Best Local Similarity 100.0%; Pred. No. 3;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 TDFTLTI 7
 CC |||||
 CC Db 13 TDFTLTI 19
 CC
 CC RESULT 11
 CC AAB97666
 CC ID AAB97666 standard; Peptide; 32 AA.
 CC AC AAB97666;
 CC DT C8-AUG-2001 (first entry)
 CC DE A33 antigen binding immunoglobulin product: VLF33 peptide SEQ ID NO:94.
 CC KW Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
 CC immunoreact; anti A33 antigen antibody; immunoglobulin.
 CC OS Homo sapiens.
 CC PN WO200131065-A1.
 CC PP 03-MAY-2001.
 CC PR 20-OCT-2000; 2000WO-US29026.
 CC PS 22-OCT-1999; 99US-2425638.
 CC PT 04-APR-2000; 2000US-0543004.
 CC PA (SCRI) SCRIPPS RES INST.
 CC PI Barbas CF, Rader C;
 CC PS WPI; 2001-328657/34.
 CC
 CC Preparing humanized rabbit antibodies that specifically immunoreact
 CC with a particular antigen using display technology for expressing
 CC libraries of antibody domains and fine tuning variable domain regions -
 CC
 CC Example 9; Page 39; 62pp; English.
 CC
 CC The present invention describes a method for preparing a humanised rabbit
 CC antibody that specifically immunoreacts with a particular antigen. The
 CC method comprises expressing a library of antibodies comprising one or
 CC more complementarity determining region (CDR) from the variable domain
 CC sequences that specifically immunoreact with the antigen grafted into
 CC framework regions from humans, and selecting the antibodies that react
 CC with the antigen. The method is useful for humanising non-human
 CC mammalian antibodies, which can be used for the treatment of a variety
 CC of diseases. The present sequence represents an A33 antigen binding
 CC immunoglobulin product VLF33 peptide which is given in an example from
 CC the present invention.
 CC

SQ Sequence 32 AA;
 Query Match 100.0%; Score 35; DB 22; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TDFTLTI 7
 |||||
 Db 13 TDFTLTI 19
 RESULT 12
 AAB97668
 ID AAB97668 standard; Peptide; 32 AA.
 AC AAB97668;
 DT 09-AUG-2001 (first entry)
 DE A33 antigen binding immunoglobulin product VLF33 peptide SEQ ID NO:94.
 KW Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
 immunoreact; anti A33 antigen antibody; immunoglobulin.
 OS Homo sapiens.
 PN WO200131065-A1.
 PP 03-MAY-2001.
 PR 20-OCT-2000; 2000WO-US29026.
 PS 22-OCT-1999; 99US-2425638.
 PT 04-APR-2000; 2000US-0543004.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Rader C;
 PS WPI; 2001-328657/34.
 Preparing humanized rabbit antibodies that specifically immunoreact
 with a particular antigen using display technology for expressing
 libraries of antibody domains and fine tuning variable domain regions -
 Example 9; Page 39; 62pp; English.
 The present invention describes a method for preparing a humanised rabbit
 antibody that specifically immunoreacts with a particular antigen. The
 method comprises expressing a library of antibodies comprising one or
 more complementarity determining region (CDR) from the variable domain
 sequences that specifically immunoreact with the antigen grafted into
 framework regions from humans, and selecting the antibodies that react
 with the antigen. The method is useful for humanising non-human
 mammalian antibodies, which can be used for the treatment of a variety
 of diseases. The present sequence represents an A33 antigen binding
 immunoglobulin product VLF33 peptide which is given in an example from
 the present invention.
 SQ Sequence 32 AA;
 Query Match 100.0%; Score 35; DB 22; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TDFTLTI 7
 |||||
 Db 13 TDFTLTI 19
 RESULT 13
 ABG98287
 ID ABG98287 standard; Peptide; 32 AA.

XX ABG98287;
XX
XX 08-JAN-2003 (first entry)
XX
XX Human antibody 012/V3b germline kappa chain variable region FR3/FR4 #1.
XX
XX Antibody: variable region; light chain; heavy chain; VH; VJ; gp39;
XX CD40; T-cell activation; B-cell differentiation; framework region;
XX cellular immune response; gene therapy; graft rejection; human; ER;
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes;
XX asthma; multiple sclerosis; allergy; diabetes mellitus;
XX systemic lupus erythematosus; graft-versus-host disease.
XX
XX Homo sapiens.
XX
XX WO200194586-A2.
XX
XX 13-DEC-2001.
XX
XX 06-JUN-2001; 2001WO-US18098.
XX
XX 06-JUN-2000; 2000US-203584P.
XX
XX (IDEC-; IDEC PHARM CORP.
XX
XX Anderson DR, Pan LZ, Hanra N, Rastetter WH, Kloetzer NS;
XX
XX WPI; 2002-198261/24.
XX
XX New antibodies binding to an epitope on gp39, useful for preventing
XX graft rejection, or for treating autoimmune diseases (e.g. diabetes,
XX asthma or multiple sclerosis), and non-autoimmune diseases (e.g.
XX graft-versus-host disease).
XX
XX Disclosure; Page 46; 130pp; English.
XX
XX The invention relates to an antibody which binds to an epitope on gp39,
XX is new, where the epitope is distinct from the epitope bound by IDEC-131,
XX and the antibody has a non-agonistic effect on T-cell activation and
XX inhibits gp39/CD40 interaction. Also included are: (1) an improved method
XX of treating a disease by modulating gp39 expression or inhibiting the
XX gp39/CD40 interaction comprising administering an antibody specific for
XX gp39 that inhibits the gp39/CD40 interaction and is non-agonistic of
XX T-cell activation; (2) an antibody which antagonises B-cell
XX differentiation and antibody production, and is non-agonistic of T-cell
XX activation; (3) a DNA sequence which encodes an antibody defined above;
XX (4) an expression vector which contains a DNA sequence of (3);
XX (5) a method of suppressing humoral and/or cellular immune responses
XX against cells or vectors administered during cell or gene therapy
XX comprising further administering prior, during or after gene therapy,
XX an antibody defined above; and (6) an improved method of treatment which
XX involves the transplantation of cells, tissues or organs of the same or
XX different species into a subject, where the improvement comprises
XX administering an antibody defined above prior, during or after
XX transplantation, to suppress immune responses against the transplanted
XX cell, tissue or organ, or to suppress immune responses elicited by the
XX transplanted cell, tissue or organ against the host. The antibody is
XX useful for preventing graft rejection, and for treating autoimmune
XX diseases, e.g., rheumatoid arthritis, multiple sclerosis, diabetes,
XX asthma, multiple sclerosis, allergic conditions, diabetes mellitus, or
XX systemic lupus erythematosus, as well as non-autoimmune diseases such as
XX graft-versus-host disease (many other diseases and conditions are
XX given in the specification). The antibodies are also useful in gene or
XX cellular therapy, and to inhibit humoral and cellular immune responses
XX against viral vectors. The present sequence is a framework region
XX (FR) fragment of a human anti-gp39 antibody used to determine which
XX amino acids should be humanised in a mouse anti-gp39 molecule.
XX
XX Sequence 32 AA;
XX
XX Query Match 100.0%; Score 35; DB 23; Length 32;
XX Best Local Similarity 100.0%; Pred. No. 3;
XX
XX Mismatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TDFLTIT 7
XX
XX DB 13 TDFLTIT 19
XX
XX RESULT 14
XX ABP62656
XX ID ABP62656 standard; Peptide; 32 AA.
XX
XX AC ABP62656;
XX
XX DT 10-OCT-2002 (first entry)
XX
XX DE Human immunopeptide to HCV E2 glycoprotein framework sequence #164.
XX
XX KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
XX nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
XX NS3 protein; viral infection.
XX
XX CS Homo sapiens.
XX
XX PK WO200259340-A1.
XX
XX PD 01-AUG-2002.
XX
XX PF 25-JAN-2002; 2002WO-US02303.
XX
XX PR 26-JAN-2001; 2001US-264451P.
XX
XX PA (SCR1) SCRIPPS RES INST.
XX
XX PI Maruyama T, Jones IM, Burton DR, Fox RI;
XX
XX WPI; 2002-599801/64.
XX
XX PT New human immunopolypeptide with binding specificity for certain
XX envelope glycoproteins and nonstructural proteins of hepatitis C virus
XX (HCV), for diagnosing or treating patients having or suspected of
XX having HCV infection.
XX
XX PS Claim 4; Fig 17; 308pp; English.
XX
XX CC The present invention relates to human immunopolypeptides, produced by a
XX phage transfected cell library. The present sequence is one such
XX immunopolypeptide. The immunopolypeptides have binding specificity for
XX envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
XX virus (HCV). E2 glycoprotein is believed to be responsible for target
XX cell binding and contains neutralising epitopes, while NS3 is thought to
XX be involved in the replication of HCV. The immunopolypeptides are useful
XX for diagnosing and treating a patient having or suspected to be having
XX HCV infection.
XX
XX SQ Sequence 32 AA;
XX
XX Query Match 100.0%; Score 35; DB 23; Length 32;
XX Best Local Similarity 100.0%; Pred. No. 3;
XX
XX Mismatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TDFLTIT 7
XX
XX DB 13 TDFLTIT 19
XX
XX RESULT 15
XX ABP62657
XX ID ABP62657 standard; Peptide; 32 AA.
XX
XX AC ABP62657;
XX
XX DT 10-OCT-2002 (first entry)
XX
XX

DE Human immunopeptide to HCV E2 glycoprotein: framework sequence #165.
XX
KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
NS3 protein; viral infection.
XX
CS Homo sapiens.
XX
PN WO200259340-A1.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-US02303.
XX
PR 26-JAN-2001; 2001US-364451P.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Maruyama T, Jones IM, Burton DR, Fox R;
XX
DR WPI; 2002-59980/64.
XX
PT New human immunopolypeptide with binding specificity for certain
envelope glycoproteins and nonstructural proteins of hepatitis C virus
(HCV), for diagnosing or treating patients having or suspected of
PT having HCV infection.
XX
XX
XX Claim 4; Fig 17; 308pp; English.
XX
XX The present invention relates to human immunopolypeptides, produced by a
phage transfected cell library. The present sequence is one such
immunopolypeptide. The immunopolypeptides have binding specificity for
envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
virus (HCV). E2 glycoprotein is believed to be responsible for target
cell binding and contains neutralising epitopes, while NS3 is thought to
be involved in the replication of HCV. The immunopolypeptides are useful
for diagnosing and treating a patient having or suspected to be having
HCV infection.
XX
XX Sequence 32 AA;

Query Match 100.0%; Score 35; DB 23; Length 32;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDETLT 7
| | | | |
Db 13 TDETLT 19

Search completed: October 4, 2003, 12:21:57
Job time : 60.3333 secs

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OX protein - protein search, using sw mode.

Run on: October 4, 2003, 12:25:27 / Search time 35.3333 Seconds
(without alignments)
21,344 Million cell updates/sec

Title: US-09-712-819C-5

Perfect score: 35

Sequence: 1 TDFTLTI 7

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 587654 seqs, 159212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA*

1: /cgn2_6/ptodata/1/pubaa/USC7_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	16	10	US-09-791-378-618
2	35	100.0	32	9	US-09-855-271-13
3	35	100.0	32	10	US-09-828-708-95
4	35	100.0	32	10	US-09-828-708-97
5	35	100.0	32	10	US-09-828-708-98
6	35	100.0	32	10	US-09-828-708-100
7	35	100.0	32	10	US-09-828-708-101
8	35	100.0	32	10	US-09-949-559-91
9	35	100.0	32	10	US-09-949-559-92
10	35	100.0	32	11	US-09-874-141-15
11	35	100.0	32	11	US-09-875-221A-91
12	35	100.0	32	11	US-09-875-221A-92
13	35	100.0	32	11	US-09-563-222-76
14	35	100.0	32	11	US-09-563-222-84
15	35	100.0	32	11	US-09-563-222-85

Sequence 116, Appl
Sequence 15, Appl
Sequence 112, Appl
Sequence 122, Appl
Sequence 57, Appl
Sequence 18, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 13, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 37, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 131, Appl
Sequence 8, Appl
Sequence 18, Appl
Sequence 114, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 15, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-09-791-378-618
; Sequence 618, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 618
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-618

Query Match 100.0%; Score 35; DB ID: Length 16;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7

Db 8 TDFTLTI 14

RESULT 2

US-09-855-271-13
; Sequence 13, Application US/09955271
; Patent No. US20020042089A1
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Mark W
; APPLICANT: Achwal, Diljeet Singh
; APPLICANT: Entage, John Spencer

; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
 ; FILE REFERENCE: CARP-0088
 ; CURRENT APPLICATION NUMBER: US/09/855,272
 ; CURRENT FILING DATE: 2001-05-15
 ; PRIOR APPLICATION NUMBER: 09/347,061
 ; PRIOR FILING DATE: 1999-07-02
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 32
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Consensus
 US-09-855-271-13

Query Match 100.0%; Score 35; DB 9; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7
 Db 13 TDFTLTI 19

RESULT 3

US-09-828-708-95
 ; Sequence 95, Application US/09828708
 ; Patent No. US20020146753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ditzel, H.
 ; APPLICANT: Burton, D.
 ; APPLICANT: Schaller, M.
 ; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their parti
 ; TITLE OF INVENTION: autoimmune disease
 ; FILE REFERENCE: 1361.005US1
 ; CURRENT APPLICATION NUMBER: US/09/828,708
 ; CURRENT FILING DATE: 2001-09-24
 ; NUMBER OF SEQ ID NOS: 123
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 95
 ; LENGTH: 32
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-828-708-95

Query Match 100.0%; Score 35; DB 10; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7
 Db 13 TDFTLTI 19

RESULT 4

US-09-828-708-97
 ; Sequence 97, Application US/09828708
 ; Patent No. US20020146753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ditzel, H.
 ; APPLICANT: Burton, D.
 ; APPLICANT: Schaller, M.

; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their parti
 ; TITLE OF INVENTION: autoimmune disease
 ; FILE REFERENCE: 1361.005US1
 ; CURRENT APPLICATION NUMBER: US/09/828,708
 ; CURRENT FILING DATE: 2001-09-24
 ; NUMBER OF SEQ ID NOS: 123
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 97
 ; LENGTH: 32
 ; TYPE: PRT

; ORGANISM: Homo sapiens
 US-09-828-708-97

Query Match 100.0%; Score 35; DB 10; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7
 Db 13 TDFTLTI 19

RESULT 5

US-09-828-708-98
 ; Sequence 98, Application US/09828708
 ; Patent No. US20020146753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ditzel, H.
 ; APPLICANT: Burton, D.
 ; APPLICANT: Schaller, M.
 ; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their parti
 ; TITLE OF INVENTION: autoimmune disease
 ; FILE REFERENCE: 1361.005US1
 ; CURRENT APPLICATION NUMBER: US/09/828,708
 ; CURRENT FILING DATE: 2001-09-24
 ; NUMBER OF SEQ ID NOS: 123
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 98
 ; LENGTH: 32
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-828-708-98

Query Match 100.0%; Score 35; DB 10; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7
 Db 13 TDFTLTI 19

RESULT 6

US-09-828-708-100
 ; Sequence 100, Application US/09828708
 ; Patent No. US20020146753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ditzel, H.
 ; APPLICANT: Burton, D.
 ; APPLICANT: Schaller, M.

; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their parti
 ; TITLE OF INVENTION: autoimmune disease
 ; FILE REFERENCE: 1361.005US1
 ; CURRENT APPLICATION NUMBER: US/09/828,708
 ; CURRENT FILING DATE: 2001-09-24
 ; NUMBER OF SEQ ID NOS: 123
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 100
 ; LENGTH: 32
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-828-708-100

Query Match 100.0%; Score 35; DB 10; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7
 Db 13 TDFTLTI 19

RESULT 7

US-09-828-708-101

; Sequence 101, Application US/09828708

; Patent No. US20020146753A1

; GENERAL INFORMATION:

; APPLICANT: Batzel, H.

; APPLICANT: Burton, D.

; APPLICANT: Schaller, M.

; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic

; FILE REFERENCE: 1361, 025US1

; CURRENT APPLICATION NUMBER: US/09/828,708

; PRIOR FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 123

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 101

; LENGTH: 32

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-828-708-101

Query Match 100.0%; Score 35; DB 10; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7

Db 13 TDFTLTI 19

RESULT 8

US-09-949-559-91

; Sequence 91, Application US/09949559

; Patent No. US20020151682A1

; GENERAL INFORMATION:

; APPLICANT: Athwal, Diljeet Singh

; APPLICANT: Brown, Derek Thomas

; APPLICANT: Weir, Andrew Neil Charles

; APPLICANT: Poppewell, Andrew George

; APPLICANT: Chapman, Andrew Paul

; APPLICANT: King, David John

; TITLE OF INVENTION: Biological Products

; FILE REFERENCE: Carp-0095

; CURRENT APPLICATION NUMBER: US/09/949,559

; PRIOR FILING DATE: 2001-12-20

; PRIOR FILING DATE: 2000-06-06

; PRIOR FILING DATE: 09/875,221

; NUMBER OF SEQ ID NOS: 130

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 91

; LENGTH: 32

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Human group 1: consensus framework 13

US-09-949-559-91

Query Match 100.0%; Score 35; DB 10; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7

Db 13 TDFTLTI 19

RESULT 9

US-09-949-559-92

; Sequence 92, Application US/09949559

; Patent No. US20020151682A1

; GENERAL INFORMATION:

; APPLICANT: Athwal, Diljeet Singh

; APPLICANT: Brown, Derek Thomas

; APPLICANT: Weir, Andrew Neil Charles

; APPLICANT: Poppewell, Andrew George

; APPLICANT: Chapman, Andrew Paul

; APPLICANT: King, David John

; TITLE OF INVENTION: Biological Products

; FILE REFERENCE: Carp-0095

; CURRENT APPLICATION NUMBER: US/09/949,559

; PRIOR FILING DATE: 2001-12-20

; PRIOR FILING DATE: 2000-06-06

; PRIOR FILING DATE: 09/875,221

; NUMBER OF SEQ ID NOS: 130

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 92

; LENGTH: 32

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: hTNF40 framework 13

US-09-949-559-92

Query Match 100.0%; Score 35; DB 10; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7

Db 13 TDFTLTI 19

RESULT 10

US-09-874-141-15

; Sequence 15, Application US/09874141

; Publication No. US20030012781A1

; GENERAL INFORMATION:

; APPLICANT: ANDERSON, DARRELL

; APPLICANT: PAN, LI-ZHEN

; APPLICANT: HANNA, NABIL

; APPLICANT: RASTETTER, WILLIAM H.

; APPLICANT: KLOETZER, WILLIAM S.

; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP19, COMPOSITIONS

; FILE REFERENCE: 037003-0280632

; CURRENT APPLICATION NUMBER: US/09/874,141

; PRIOR FILING DATE: 2001-06-06

; PRIOR FILING DATE: 60/209,584

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 15

; LENGTH: 32

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-874-141-15

Query Match 100.0%; Score 35; DB 11; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDFTLTI 7

Db 13 TDFTLTI 19

RESULT 11

US-09-875-221A-91

; Sequence 91, Application US/09875221A

; Publication No. US20030026805A1

; GENERAL INFORMATION:

; APPLICANT: Athwal, Diljeet Singh

; APPLICANT: Brown, Derek Thomas

```

; APPLICANT: Weir, Andrew Neil Charles
; APPLICANT: Popplewell, Andrew George
; APPLICANT: Chapman, Andrew Paul
; APPLICANT: King, David John
; TITLE OF INVENTION: Biocological Products
; FILE REFERENCE: Carp-0089
; CURRENT APPLICATION NUMBER: US/09/875,221A
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: GB00138-0.7
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human group 1 consensus framework L3
US-09-875-221A-91

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Query Match      100.0%; Score 35; DB 11; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 TDFLTII 7
    |||||
Db 13 TDFLTII 19

```

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RESULT 12
US-09-875-221A-92
; Sequence 92, Application US/09875221A
; Publication No. US2003026805A1
; GENERAL INFORMATION:
; APPLICANT: Atwal, Diljeet Singh
; APPLICANT: Brown, Derek Thomas
; APPLICANT: Weir, Andrew Neil Charles
; APPLICANT: Popplewell, Andrew George
; APPLICANT: Chapman, Andrew Paul
; APPLICANT: King, David John
; TITLE OF INVENTION: Biological Products
; FILE REFERENCE: Carp-0089
; CURRENT APPLICATION NUMBER: US/09/875,221A
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: GB0013810.7
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KTNF4C framework L3
US-09-875-221A-92

```

```

Query Match      100.0%; Score 35; DB 11; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 TDFLTII 7
    |||||
Db 13 TDFLTII 19

```

```

RESULT 13
US-09-563-222-76
; Sequence 76, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN

```

```

; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-76

```

```

Query Match      100.0%; Score 35; DB 11; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 TDFLTII 7
    |||||
Db 13 TDFLTII 19

```

```

RESULT 14
US-09-563-222-84
; Sequence 84, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-84

```

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Query Match      100.0%; Score 35; DB 11; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 TDFLTII 7
    |||||
Db 13 TDFLTII 19

```

```

RESULT 15
US-09-563-222-88
; Sequence 88, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-88

```

```

Query Match      100.0%; Score 35; DB 11; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TDFTLT 7
111111
Db 13 TDFTLT 19

Search completed: October 4, 2003, 12:42:33
Job time : 36.333 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

DM protein - protein search, using sw model

Run on: October 4, 2003, 12:18:51 ; Search time 17.6667 Seconds
(without alignments)
16.765 Million cell updates/sec

Title: US-09-712-819C-5

Perfect score: 35

Sequence: 1 TDFTLTI 7

Scoring table: BLCSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4213858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA.*

- 1: /cgn2_6/prodata/1/aa/5A.COMB.pep.*
- 2: /cgn2_6/prodata/1/aa/5B.COMB.pep.*
- 3: /cgn2_6/prodata/1/aa/6A.COMB.pep.*
- 4: /cgn2_6/prodata/1/aa/6B.COMB.pep.*
- 5: /cgn2_6/prodata/1/aa/6CTUS.COMB.pep.*
- 6: /cgn2_6/prodata/1/aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	25	5	PCT-US91-02942-42
2	35	100.0	32	2	US-08-470-139-13
3	35	100.0	32	3	US-08-569-147-40
4	35	100.0	32	4	US-09-347-061-13
5	35	100.0	32	4	US-09-425-638A-92
6	35	100.0	32	4	US-09-425-638A-94
7	35	100.0	32	4	US-09-543-004-92
8	35	100.0	32	4	US-09-543-004-94
9	35	100.0	50	5	PCT-US91-02942-9
10	35	100.0	52	1	US-08-162-102C-43
11	35	100.0	54	2	US-08-162-102C-44
12	35	100.0	64	2	US-08-765-173B-10
13	35	100.0	64	2	US-08-765-173B-14
14	35	100.0	70	3	US-08-554-840-9
15	35	100.0	70	4	US-08-925-339-9
16	35	100.0	70	4	US-09-332-595-9
17	35	100.0	76	3	US-08-851-362D-21
18	35	100.0	79	3	US-08-554-840-14
19	35	100.0	79	4	US-08-925-339-14
20	35	100.0	79	4	US-09-332-595-14
21	35	100.0	80	3	US-08-554-840-12
22	35	100.0	80	3	US-08-554-840-13
23	35	100.0	80	3	US-08-554-840-15
24	35	100.0	80	4	US-08-925-339-12
25	35	100.0	80	4	US-08-925-339-13
26	35	100.0	80	4	US-08-925-339-15
27	35	100.0	80	4	US-09-332-595-12

28	35	100.0	80	4	US-09-332-595-13	Sequence 13, Appl
29	35	100.0	80	4	US-09-332-595-15	Sequence 15, Appl
30	35	100.0	81	3	US-08-554-840-11	Sequence 11, Appl
31	35	100.0	81	4	US-08-925-339-11	Sequence 11, Appl
32	35	100.0	81	4	US-09-332-595-11	Sequence 11, Appl
33	35	100.0	91	2	US-08-373-146-49	Sequence 49, Appl
34	35	100.0	91	1	US-08-276-852-111	Sequence 111, App
35	35	100.0	93	1	US-08-399-575-111	Sequence 111, App
36	35	100.0	93	1	US-08-899-575-111	Sequence 111, App
37	35	100.0	93	3	US-08-783-853A-33	Sequence 33, Appl
38	35	100.0	93	4	US-09-344-050-35	Sequence 35, Appl
39	35	100.0	93	5	PCT-US95-08743-111	Sequence 111, App
40	35	100.0	96	3	US-08-466-368-6	Sequence 6, Appl
41	35	100.0	96	4	US-08-470-998-3	Sequence 3, Appl
42	35	100.0	99	4	US-09-639-896-6	Sequence 6, Appl
43	35	100.0	99	4	US-09-893-896-10	Sequence 10, Appl
44	35	100.0	100	4	US-09-493-896-2	Sequence 2, Appl
45	35	100.0	100	4	US-09-893-896-4	Sequence 4, Appl

ALIGNMENTS

RESULT :
PCT-US91-02942-42
Sequence 42, Application: PC/TUS9102942
GENERAL INFORMATION:
APPLICANT: ROTHLEIN, ROBERT
APPLICANT: ADAIR, JOHN R
TITLE OF INVENTION: HUMANIZED CHR-GRAFTED ICAM-1 ANTIBODY
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steine, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Ave. NW Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02942
FILING DATE: 19910429
CLASSIFICATION: 415
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9009549.8
FILING DATE: 27-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: FOX, SAM L
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1011-0596600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-02942-42

Query Match 100.0% Score 35; DB 5; Length 25;
Best Local Similarity 100.0%; Pred No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TDFTLTI 7
DB 6 TDFTLTI 12

RESULT 2
US-08-470-139-13
Sequence 13, Application US/08470139
Patent No. 598696
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies
NUMBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPC)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,139
FILING DATE: 26 JUNE-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TRUJILLO, DOREEN YATKO
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0044
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-470-139-13

Query Match 100.0%; Score 35; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
DB 13 TDFTLTI 19

RESULT 3
US-08-569-147-40
Sequence 40, Application US/08569147
Patent No. 6180377
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMANISED ANTIBODIES
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSER: No. 618037715, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPC)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,147
FILING DATE: 25-March-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3300
TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-569-147-40

Query Match 100.0%; Score 35; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
DB 13 TDFTLTI 19

RESULT 4
US-09-347-061-13
Sequence 13, Application US/09347061
Patent No. 6316227
GENERAL INFORMATION:
APPLICANT: Bodmer, Mark
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Emage, John Spencer
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
FILE REFERENCE: CARP-0071
CURRENT APPLICATION NUMBER: US/09/347,061
CURRENT FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 13
LENGTH: 32
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Consensus
US-09-347-061-13

Query Match 100.0%; Score 35; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
DB 13 TDFTLTI 19

RESULT 5
US-09-425-638A-92
Sequence 92, Application US/09425638A
Patent No. 6342587
GENERAL INFORMATION:
APPLICANT: Carlos F. Barbas III, Christopher Rader, Gerd Ritter, Sydney Welt and
APPLICANT: Lloyd J. Old
TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
FILE REFERENCE: LJD 5630
CURRENT APPLICATION NUMBER: US/09/425,638A
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 129
SEQ ID NO: 92
LENGTH: 32
TYPE: PRI
ORGANISM: Homo sapiens
FEATURE:
US-09-425-638A-92

Query Match 100.0%; Score 35; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 TDFTLTI 7
|||||||
b 13 TDFTLTI 19

RESULT 6

S-09-425-638A-94

Sequence 94, Application US/09425638A

Patent No. 6342587

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and

APPLICANT: Lloyd J. Old

TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF

FILE REFERENCE: LUD 5630

CURRENT APPLICATION NUMBER: US/09/425.638A

CURRENT FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 94

LENGTH: 32

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

S-09-425-638A-94

Query Match

Best Local Similarity 100.0%; Score 35; DB 4; Length 32;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 TDFTLTI 7

|||||||

b 13 TDFTLTI 19

RESULT 7

S-09-543-004-92

Sequence 92, Application US/09543004

Patent No. 6346249

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and

APPLICANT: Lloyd J. Old

TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF

FILE REFERENCE: LUD 5630.1

CURRENT APPLICATION NUMBER: US/09/543.004

CURRENT FILING DATE: 2000-04-04

PRIOR APPLICATION NUMBER: C9/425.638

PRIOR FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 92

LENGTH: 32

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

S-09-543-004-92

Query Match

Best Local Similarity 100.0%; Score 35; DB 4; Length 32;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 TDFTLTI 7

|||||||

b 13 TDFTLTI 19

RESULT 8

S-09-543-004-94

Sequence 94, Application US/09543004

Patent No. 6346249

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and

APPLICANT: Lloyd J. Old

TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF

FILE REFERENCE: LUD 5630.1

CURRENT APPLICATION NUMBER: US/09/543.004

Y 1 TDFTLTI 7
|||||||
b 13 TDFTLTI 19

Y 1 TDFTLTI 7
|||||||
b 13 TDFTLTI 19

Y 1 TDFTLTI 7
|||||||
b 13 TDFTLTI 19

Y 1 TDFTLTI 7
|||||||
b 13 TDFTLTI 19

Y 1 TDFTLTI 7
|||||||
b 13 TDFTLTI 19

Y 1 TDFTLTI 7
|||||||
b 13 TDFTLTI 19

RESULT 9

PCT-US91-02942-9

Sequence 9, Application PC/TUS9102942

GENERAL INFORMATION:

APPLICANT: ROTHLEIN, ROBERT

APPLICANT: ADAIR, JOHN R

APPLICANT: AHWAL, DILJEET S

TITLE OF INVENTION: HUMANIZED CDR-GRAFTED IGHM-1 ANTIBODY

NUMBER OF SEQUENCES: 102

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox

STREET: 1225 Connecticut Ave. NW Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DCS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/02942

FILING DATE: 19910429

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9009549.8

FILING DATE: 27-APR-1990

ATTORNEY/AGENT INFORMATION:

NAME: FOX, SAM L

REGISTRATION NUMBER: 30,353

REFERENCE/DOCKET NUMBER: 1011.0596600

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 466-0800

TELEFAX: (202) 433-8716

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 50 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US91-02942-9

Y 1 TDFTLTI 7
|||||||
b 24 TDFTLTI 30

Y 1 TDFTLTI 7
|||||||
b 24 TDFTLTI 30

Y 1 TDFTLTI 7
|||||||
b 24 TDFTLTI 30

Y 1 TDFTLTI 7
|||||||
b 24 TDFTLTI 30

RESULT 10

US-08-162-102C-43
Sequence 43, Application US/08162102C
Patent No. 5762905
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R.
APPLICANT: Barbas, III, Carlos F.
APPLICANT: Chanock, Robert M.
APPLICANT: Murphy, Brian R.
APPLICANT: Crowe, Jr., James E.
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TO RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-162-102C
FILING DATE: 10-DEC-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07300/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-162-102C-43

Query Match 100.0%, Score 35; DB 1; Length 52;
Best Local Similarity 100.0%, Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
DB 13 TDFTLTI 19

RESULT 11
US-08-162-102C-44
Sequence 44, Application US/08162102C
Patent No. 5762905
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R.
APPLICANT: Barbas, III, Carlos F.
APPLICANT: Chanock, Robert M.
APPLICANT: Murphy, Brian R.
APPLICANT: Crowe, Jr., James E.
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TO RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,102C
FILING DATE: 10-DEC-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07300/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-162-102C-44

Query Match 100.0%, Score 35; DB 1; Length 53;
Best Local Similarity 100.0%, Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTI 7
DB 13 TDFTLTI 19

RESULT 12
US-08-765-179B-10
Sequence 10, Application US/08765179B
Patent No. 5854027
GENERAL INFORMATION:
APPLICANT: STEIPE, Boris
APPLICANT: STEINBACHER, Stefan
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
OF ANTIBODIES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikolaide, Martelstein, Murray & Gram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,179B
FILING DATE: 14-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02626
FILING DATE: 06-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 2 44 25 15.7
FILING DATE: 15-JUL-1994
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

S-08-765-179B-10

Query Match 100.0%; Score 35; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 TDFTLTI 7
b 38 TDFTLTI 44

RESULT 13

S-08-765-179B-14

Sequence 14, Application US/08765179B

Patent No. 5854327

GENERAL INFORMATION:

APPLICANT: STEIFE, Boris

APPLICANT: STEINACHER, Stefan

TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY

TITLE OF INVENTION: OF ANTIBODIES

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP

STREET: 655 Fifteenth Street N.W. Suite 310

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/765,179B

FILING DATE: 14-JAN-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/02626

FILING DATE: 06-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 25 115.7

FILING DATE: 15-JUL-1994

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 64 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

S-08-765-179B-14

Query Match 100.0%; Score 35; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 TDFTLTI 7
b 38 TDFTLTI 44

RESULT 14

S-08-554-840-9

Sequence 9, Application US/08554840

Patent No. 6001358

GENERAL INFORMATION:

APPLICANT: BLACK, Amelia

APPLICANT: HANNA, Nabil

APPLICANT: PADLAN, Eduardo A.

APPLICANT: NEWMAN, Roland A.

TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp19,

TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/554,840

FILING DATE: 07-NOV-1995

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-127

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 70 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-554-840-9

Query Match 100.0%; Score 35; DB 3; Length 70;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 TDFTLTI 7

b 51 TDFTLTI 57

RESULT 15

US-08-925-339-9

Sequence 9, Application US/08925339

Patent No. 6440418

GENERAL INFORMATION:

APPLICANT: BLACK, Amelia

APPLICANT: HANNA, Nabil

APPLICANT: PADLAN, Eduardo A.

APPLICANT: NEWMAN, Roland A.

TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp19,

TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/925,339

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/554,840

FILING DATE: 07-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.
 REGISTRATION NUMBER: 35,030
 REFERENCE/SOCKET NUMBER: C12712-127
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6620
 TELEFAX: (703) 836-2021
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 70 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-925-339-9

Query Match 100.0%; Score 35; EE 4; Length 70;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFILTI 7
 1 1 1 1 1 1 1
 DB 51 TDFILTI 57

Search completed: October 4, 2003, 12:27:22
 Job time : 18.6667 secs

Result No.	Query	Score	Match		Length	DB	ID	Description
			Match					
1	33	100.0	54	2	S34093		IG kappa chair. V r	
2	33	100.0	71	2	H30538		IG kappa chair. V r	
3	33	100.0	72	2	S40358		IG kappa chair. V r	
4	33	100.0	75	2	S40337		IG kappa chair. V r	
5	33	100.0	83	2	S34095		IG kappa chair. V r	
6	33	100.0	83	2	S24211		IG kappa chair. V r	
7	33	100.0	87	2	S34091		IG kappa chair. V r	
8	33	100.0	87	2	S24594		IG kappa chair. V r	
9	33	100.0	89	2	B25155		IG kappa chair. V r	
10	33	100.0	91	2	S42186		IG kappa chair. V r	
11	33	100.0	91	2	S25463		IG kappa chair. V r	
12	33	100.0	93	2	PH1039		IG light chair. V r	
13	33	100.0	94	2	PL0258		IG kappa chair. V r	
14	33	100.0	96	2	S46320		IG kappa chair. V r	
15	33	100.0	99	2	S24501		IG kappa chair. V r	
16	33	100.0	99	2	E28833		IG heavy chair. V r	
17	33	100.0	99	2	S24504		IG kappa chair. V r	
18	33	100.0	100	2	S26334		IG light chair. V r	
19	33	100.0	100	2	S24681		IG kappa chair. V r	
20	33	100.0	102	2	S45440		IG kappa chair. V r	
21	33	100.0	101	2	PH1057		IG light chair. V r	
22	33	100.0	101	2	C34153		IG kappa chair. V r	
23	33	100.0	101	2	A33730		IG kappa chair. V r	
24	33	100.0	102	2	PH1035		IG light chair. V r	
25	33	100.0	102	2	PH1044		IG light chair. V r	
26	33	100.0	102	2	S14592		IG kappa chair. V r	
27	33	100.0	102	2	E28195		IG kappa chair. V r	
28	33	100.0	102	2	S14594		IG kappa chair. V r	
29	33	100.0	102	2	S14593		IG kappa chair. V r	

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Fi:50/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 33; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
DB 61 FTLKISR 67

RESULT 6
S24211
Ig kappa chain V region (V3a) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24211
R:Parfent, W.; Meindl, A.; Thiebe, R.; Mitzel, S.; Zachau, H.G.
Eur. J. Immunol. 21, 1821-1827, 1991
A:Title: The human immunoglobulin kappa locus. Characterization of the duplicated C kappa
A:Reference number: S24205; MUID:91330953; PMID:1907917
A:Accession: S24211
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-83 <PAR>
A:Cross-references: EMBL:X59317; NID:933270; PID:CAA4204.1; PID:933271
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match      100.0%; Score 33; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
DB 59 FTLKISR 65

RESULT 7
S34091
Ig kappa chain V region (patient 19 and 20) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: S34091; S34092
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34091
A:Molecule type: DNA
A:Residues: 1-87 <WAG>
A:Cross-references: EMBL:X67175
A:Experimental source: patient 19
A:Accession: S34092
A:Molecule type: DNA
A:Residues: 1-87 <WAG>
A:Cross-references: EMBL:X67176
A:Experimental source: patient 20
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:3-82/Domain: immunoglobulin homology <IMV>

Query Match      100.0%; Score 33; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
DB 63 FTLKISR 69

RESULT 8
S34094
Ig kappa chain V region (patient 19 and 20) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: S34091; S34092
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34095
A:Molecule type: DNA
A:Residues: 1-83 <WAG>
A:Cross-references: EMBL:X67179
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
```

PL0258
IG kappa chain V region (anti-DNA, 128-VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)

Residues: 1-91 <MO1>
Cross-references: EMBL:Z2542; N.D.G497830; P.D.N.CA93329.1; P.D.G497831
Note: the authors translated the codon GTT for residue 81 as Thr, TGS for residue 85 as
Accession: S42195
Status: preliminary
Molecule type: DNA
Residues: 1-91 <MO2>

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C:Accession: P10258
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-6/Region: framework 1
 F:7-22/Region: complementarity-determining 1
 F:23-37/Region: complementarity-determining 2
 F:38-44/Region: complementarity-determining 2
 F:45-76/Region: framework 3
 F:77-85/Region: complementarity-determining 3
 F:86-94/Region: framework 4
 A:Molecule type: mRNA
 A:Residues: 1-94 <SL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-6/Region: framework 1
 F:7-22/Region: complementarity-determining 1
 F:23-37/Region: complementarity-determining 2
 F:38-44/Region: complementarity-determining 2
 F:45-76/Region: framework 3
 F:77-85/Region: complementarity-determining 3
 F:86-94/Region: framework 4
 A:Molecule type: mRNA
 A:Residues: 1-94 <SL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-6/Region: framework 1
 F:7-22/Region: complementarity-determining 1
 F:23-37/Region: complementarity-determining 2
 F:38-44/Region: complementarity-determining 2
 F:45-76/Region: framework 3
 F:77-85/Region: complementarity-determining 3
 F:86-94/Region: framework 4
 A:Molecule type: mRNA
 A:Residues: 1-94 <SL>

Query Match 100.0%; Score 33; DB 2; Length 94;

Best Local Similarity 100.0%; Pred. No. 0.77; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : FTLKISR 7

DB 59 FTLKISR 65

RESULT 14

S40320
 Ig kappa chain - human
 C:Species: Homo sapiens (man)
 C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1993
 C:Accession: S40320
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A:Reference number: S40312; MUID:94060891; PMID:9258341
 A:Accession: S40320
 A>Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-96 <KLE>
 A:Cross-references: EMBL:X72430; NID:9441328; FIRM:CAA1095.1; PID:944128
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 96;

Best Local Similarity 100.0%; Pred. No. 0.79; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : FTLKISR 7

DB 59 FTLKISR 65

RESULT 15

S24501
 Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
 C:Accession: S24501
 R:Kaartinen, M.
 submitted to the EMBL Data Library, October 1991
 A:Reference number: S24490
 A:Accession: S24501
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-99 <KAA>
 A:Cross-references: EMBL:X66638
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-95/Domain: immunoglobulin homology <INX>

Query Match 100.0%; Score 33; DB 2; Length 99;

Best Local Similarity 100.0%; Pred. No. 0.82; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : FTLKISR 7

DB 75 FTLKISR 82

Search completed: October 4, 2003, 12:26:21

Cob time : 20.3333 secs.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:09:51 ; Search time 10.6667 Seconds
(without alignments)
30.861 Million cell updates/sec

Title: US-09-712-819C-6

Perfect score: 33

Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 3.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_4.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	112	1 KV2C HUMAN	P01616 hmo sapien
2	33	100.0	113	1 KV2D HUMAN	P01617 hmo sapien
3	33	100.0	113	1 KV2G MOUSE	P01631 mus musculu
4	33	100.0	115	1 KV2A HUMAN	P01614 hmo sapien
5	33	100.0	117	1 KV2E HUMAN	P06309 hmo sapien
6	33	100.0	133	1 KV2F HUMAN	P06310 hmo sapien
7	30	90.9	112	1 KV2D MOUSE	P01629 mus musculu
8	30	90.9	113	1 KV2B HUMAN	P01615 hmo sapien
9	30	90.9	113	1 KV2E MOUSE	P03976 mus musculu
10	30	90.9	113	1 KV2F MOUSE	P01630 mus musculu
11	30	90.9	512	1 ANM3 HUMAN	O60678 hmo sapien
12	30	90.9	772	1 CIPB CLOTH	Q01966 clostridium
13	30	90.9	1953	1 CIPA CLOTH	Q06851 clostridium
14	29	87.9	112	1 KV2A MOUSE	P01626 mus musculu
15	29	87.9	113	1 KV2C MOUSE	P01628 mus musculu
16	29	87.9	120	1 KV2S MOUSE	P01627 mus musculu
17	29	87.9	834	1 PLSB PSEAE	Q9Hxw7 pseudomonas
18	28	84.8	259	1 Y6B8 CHLRE	O84071 chlamydia t
19	28	84.8	259	1 Y339 CHLMC	Q9Pxx1 chlamydia m
20	28	84.8	711	1 CAD2 LISMO	Q60348 listeria mo
21	28	84.8	745	1 ATK2 ARATH	P46864 arabidopsis
22	27	81.8	100	1 KV3C HUMAN	P01621 hmo sapien
23	27	81.8	108	1 KV3A HUMAN	P01619 hmo sapien
24	27	81.8	109	1 KV3B HUMAN	P01620 hmo sapien
25	27	81.8	109	1 KV3D HUMAN	P01622 hmo sapien
26	27	81.8	109	1 KV3E HUMAN	P01623 hmo sapien
27	27	81.8	109	1 KV3G HUMAN	P04206 hmo sapien
28	27	81.9	127	1 Y067 YEAST	P47105 saccharomyc
29	27	81.8	129	1 KV3H HUMAN	P04207 hmo sapien
30	27	81.8	129	1 KV3L HUMAN	P18135 hmo sapien
31	27	81.8	129	1 KV3M HUMAN	P18136 hmo sapien
32	27	81.8	295	1 YH08 YEAST	P38805 saccharomyc
33	27	81.8	299	1 ATNC_BURVA	P33002 bufo marinu

ALIGNMENTS

RESULT 1
KV2C_HUMAN ID KV2C_HUMAN STANDARD; PRT; 112 AA.
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 15-kappa chain V-II region ML.
CS Homo sapiens (Human).
CC Exaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID:9606;
RN 11;
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis";
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; AC1887; K2HML.
DR HSP; P80362; IWT.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR0031006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE491 CRC64;

Query Match 100.0%; Score 33; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DQ .75 FTLKISR 81

RESULT 2
KV2D_HUMAN ID KV2D_HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

P22839 proteus mir
Q9CIX3 pasteurella
P35774 mus musculu
Q95239 homo sapien
Q95400 homo sapien
QJ7310 rattus norv
P01618 drosophila
Q8K7X4 carnis famil
Q8PLF4 streptococc
P58183 streptococc
P50361 rhizobium s

Ig kappa chain, V-II region, TEW.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE (BENCE-JONES PROTEIN TEW).
MEDLINE=74148480; PubMed=4596149;
Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.:
"Amino acid sequence of a kappa Bence Jones protein from a case of
primary amyloidosis.";
Biochemistry 12:3763-3780 (1973).
[2]
SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
MEDLINE=73166618; PubMed=4720495;
Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
Glenner G.G.:
"Structural identity of Bence Jones and amyloid fibril proteins in a
patient with plasma cell dyscrasia and amyloidosis.";
J. Clin. Invest. 52:1276-1281 (1973).
-!- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
-!- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
PATIENT WITH PLASMA CELL DYSKRASIA AND AMYLOIDOSIS.
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1.2)
MARKER.
PIR: A90370; K2HUTW.
HSSP: P01607; 1REI.
GO: GO:0005576; C:extracellular; NAS.
GO: GO:0003823; P:antigen binding activity; NAS.
GO: GO:0006955; P:immune response; NAS.
InterPro: IPR007110; Ig-like.
InterPro: IPR003096; Ig MHC.
InterPro: IPR003596; Ig_V.
Pfam: PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG_LIKE; 1.
Immunoglobulin V region; Bence-Jones protein; Amyloid.
DOMAIN 1 23
DOMAIN 24 39
COMPLEMENTARITY-DETERMINING-1.
DOMAIN 40 54
COMPLEMENTARITY-DETERMINING-2.
DOMAIN 55 61
COMPLEMENTARITY-DETERMINING-3.
DOMAIN 62 93
COMPLEMENTARITY-DETERMINING-4.
DOMAIN 94 102
DISULFID 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; 0C3C38F81F843CA CRC64;
Query Match 100.0%; Score 33; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
DB 76 FTLKISR 82

Query Match 100.0%; Score 33; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
DB 76 FTLKISR 82

RESULT 4
KV2A_HUMAN STANDARD; PRT; 115 AA.
AC P0614;
CT 21-JUL-1986 (Rel. 01, Created)
CT 21-JUL-1986 (Rel. 01, Last sequence update)
CT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region C-um.
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CX NCBI_TaxID=9606;
RN 1;
RV SEQUENCE.
RP MEDLINE=68242259; PubMed=5586923;
RX Hilschmann N.;
RA "The complete amino acid sequence of Bence Jones protein C-um (kappa-
type).";
RT Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722 (1967).
RN 2;
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70083440; PubMed=4188189;
RA Hilschmann N.;
RA "Molecular basis of antibody formation.";
RT Naturwissenschaften 56:195-205 (1969).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: B91639; K2HUCM.
DR HSSP: P01607; 1REI.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003096; Ig MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.


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DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
WT DISULFID 24 95
  BY SIMILARITY.
  NON TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match      100.0%; Score 33; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 FTLKISR 7
   |||||
Db 78 FTLKISR 84

RESULT 5
KV2F HUMAN
ID KV2F HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DI 01-JAN-1988 (Rel. 06, Last sequence update)
DI 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Frag-ent).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84197506; PubMed=4325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa II germ-line genes to light-chain
  diversity.";
RL Nature 309:73-76 (1984).

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  or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z00309; ; NOT_ANNOTATED_CDS.
CC PIR; A01889; K2HJGM.
CC HSSP; P80362; LWTJ.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; P:antigen binding activity; NAS.
CC GO; GO:0003695; P:immune response; NAS.
CC InterPro; IPR007110; IG_LIKE.
CC InterPro; IPR003006; IG_MHC.
CC Pfam; PF00047; IG_1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
CC NON TER 1 1
CC SIGNAL <1 4
CC CHAIN 5 117
CC DOMAIN 5 27
CC DOMAIN 28 43
CC DOMAIN 44 58
CC DOMAIN 59 65
CC DOMAIN 66 97
CC DOMAIN 98 106
CC DOMAIN 107 116
CC DISULFID 27 97
CC NON TER 117 117
CC SEQUENCE 117 AA; 12664 MW; 92C57DC713E558B1 CRC64;

Query Match      100.0%; Score 33; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 FTLKISR 7
   |||||
Db 80 FTLKISR 86

RESULT 6
KV2F HUMAN
ID KV2F HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DI 01-JAN-1988 (Rel. 06, Last sequence update)
DI 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2897711;
RA Klobbeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
  III.";
RL Nucleic Acids Res. 13:6499-6513 (1985).

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CC -----
CC EMBL; Z00020; CAA77315.1;
CC PIR; A01890; K2HURP.
CC HSSP; P80382; LWTJ.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; P:antigen binding activity; NAS.
CC GO; GO:0003695; P:immune response; NAS.
CC InterPro; IPR007110; IG_LIKE.
CC InterPro; IPR003006; IG_MHC.
CC InterPro; IPR003596; IG_V.
CC Pfam; PF00047; IG_1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 20
CC CHAIN 21 133
CC DOMAIN 21 43
CC DOMAIN 44 59
CC DOMAIN 60 74
CC DOMAIN 75 81
CC DOMAIN 82 113
CC DOMAIN 114 122
CC DOMAIN 123 132
CC DISULFID 43 113
CC NON TER 133 133
CC SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match      100.0%; Score 33; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
Db 96 FTLKISR 102

RESULT 7
KV2D MOUSE
ID KV2D MOUSE STANDARD; PRT; 112 AA.
AC P01629;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 2S1.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=833555.01; PubMed=7141411;
RA Herbst H., Chang J.Y., Abersold R., Braun D.G.;
RT "Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for
ST the group A streptococcal polysaccharide.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).
CC -!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTI-BODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
CC
CC PIR; A01911; KVM331.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003056; Ig_MHC.
DR InterPro; IPR003056; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region; Monoclonal antibody.
KW DOMAIN 1 23
FT DOMAIN 24 39
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54
FT FRAMEWORK-2.
FT DOMAIN 55 61
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93
FT FRAMEWORK-3.
FT DOMAIN 94 102
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112
FT FRAMEWORK-4.
FT DISULFID 23 93
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12221 MW; BD3EF56D789FEEC CRC64;

Query Match 90.9%; Score 30; DB 1; Length 112;
Best Local Similarity 85.7%; Pred. No. 2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 76 FTLKISR 82

RESULT 8
KV2B_HUMAN STANDARD; PRT; 113 AA.
AC P01615;
CD 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76253627; PubMed=821524;
RA Riesen W.F., Jaton J.-C.;
RT "Variable region: sequence of the light chain from a Waldenström's IgM
RT with specificity for phosphorylcholine.";
RL Biochemistry 15:3829-3833(1976).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC -!- MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
CC
CC PIR; A01886; K2HUF8.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; Extracellular; NAS.
DR GO; GO:0003823; Antigen binding activity; NAS.
DR GO; GO:0006955; Immune response; NAS.
DR InterPro; IPR007110; Ig-like.

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DR InterPro; IPR003006; Ig_MEC.
DR InterPro; IPR003056; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT FRAMEWORK-1.
FT DOMAIN 24 39
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54
FT FRAMEWORK-2.
FT DOMAIN 55 61
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93
FT FRAMEWORK-3.
FT DOMAIN 94 102
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112
FT FRAMEWORK-4.
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46D596BE CRC64;

Query Match 90.9%; Score 30; DB 1; Length 113;
Best Local Similarity 85.7%; Pred. No. 2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 76 FTLKISR 82

RESULT 9
KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
CD 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX TISSUE=Hybridoma;
RX MEDLINE=8512868; PubMed=6441768;
RA Abersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6
RT origin: monoclonal antibodies 17S29.1 and 22S25.1: specific for the
RT group A streptococcal polysaccharide.";
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -!- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTI-BODY.
CC
CC PIR; A01912; KVM517.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003056; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT FRAMEWORK-1.
FT DOMAIN 24 39
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54
FT FRAMEWORK-2.
FT DOMAIN 55 61
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93
FT FRAMEWORK-3.
FT DOMAIN 94 102
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112
FT FRAMEWORK-4.
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797C46F8D533 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 113;
Best Local Similarity 85.7%; Pred. No. 2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7

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Db 76 FTLRIS E2
|||||
RESULT 10
KV2F MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 7S34.1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10290;
OR X
CC [1]
SEQUENCE
MEDLINE=83256427; PubMed=6409068;
Chang J.-Y., Herbst R., Aebersold R., Braun E.G.;
"A new isotype sequence (V kappa 27) of the variable region of kappa-
light chains from a mouse hybridoma-derived anti-(streptococcal group
A polysaccharide) antibody containing an additional cysteine residue.
Application of the dimethylaminoazobenzene isothiocyanate technique
for the isolation of peptides."
Biochem. J. 211:173-180(1983).
-!- MISCELLANEOUS; THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
PIR; A01913; KVM378.
DR HSSP; E80362; LNW.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR033066; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00647; Ig_1.
DR SMART; SMC0406; Ig_v_1.
DR PROSITE; PS00935; IG_LIKE; 1.
<KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
DOMAIN 1 23
FRAMEWORK-1.
-!- DOMAIN 24 39
COMPLEMENTARITY-DETERMINING-1.
-!- DOMAIN 40 54
FRAMEWORK-2.
-!- DOMAIN 55 61
COMPLEMENTARITY-DETERMINING-2.
-!- DOMAIN 62 73
FRAMEWORK-3.
-!- DOMAIN 94 102
COMPLEMENTARITY-DETERMINING-3.
-!- DOMAIN 103 112
FRAMEWORK-4.
-!- DISULFID 23 93
BY SIMILARITY.
FT NON_TER 113 113
SEQUENCE 113 AA; 12496 MW; 42CG19D1CADA3C91 CRC64;
Query Match 90.9%; Score 30; DB 1; Length 113;
Best Local Similarity 85.7%; Pred. NC. 2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CY 1 FTLKISR 7
|||||
Db 76 FTLRIS 82
|||||
RESULT 11
ANM3 HUMAN STANDARD; PRT; 512 AA.
AC C60678;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein arginine N-methyl-transferase 3 (EC 2.1.1.1) (Fragment).
CN PRM13
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
OR X
CC [1]
SEQUENCE FROM N.A.
MEDLINE=9642256; PubMed=9642256;
Tang J., Gary J.D., Clarke S., Herschman H.R.;
"PRMT 3, a type I protein arginine N-methyltransferase that differs
from PRMT1 in its oligomerization, subcellular localization,
substrate specificity, and regulation."
J. Biol. Chem. 273:16935-16945(1998).
-!- FUNCTION: METHYLATES (MONO AND ASYMMETRIC DIMETHYLATION) THE
GUANIDINO NITROGENS OF ARGINYL RESIDUES IN SOME PROTEINS.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE PROTEIN ARGININE N-METHYLTRANSFERASE
FAMILY.
-----
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-----
CC EMBL; AF059531; AAC39837.1; -.
DR XIM; 603190; -.
DR GO; GO:0005737; Cytoplasm; NAS.
DR GO; GO:0016274; F-protein-arginine N-methyltransferase activity; NAS.
DR InterPro; IPR000051; SAM_bind.
DR InterPro; IPR007087; Znf_C2H2.
DR SMART; SM00355; Znf_C2H2; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
KW Transferase; Methyltransferase; Zinc-finger.
FT NON_TER 1 52
FT ZN_FING 29 52 C2H2-TYPE.
SQ SEQUENCE 512 AA; 58098 MW; 260DC4EB25162A18 CRC64;
Query Match 90.9%; Score 30; DB 1; Length 512;
Best Local Similarity 85.7%; Pred. NC. 9.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CY 1 FTLKISR 7
|||||
Db 419 FTLKISR 425
|||||
RESULT 12
CIPB CLOTM STANDARD; PRT; 772 AA.
AC C01866;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellulosomal scaffolding protein B (Cellulosomal glycoprotein S1/SL)
DE (Cellulose integrating protein B) (Fragment).
GN CIPB.
OS Clostridium thermocellum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1515;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS.
RX MEDLINE=93146373; PubMed=1490597;
RA Poole J.W., Morag E., Lamed R., Bayer E.A., Hazlewood G.P.,
RA Gilbert H.J.;
RT subunit S1 from Clostridium thermocellum YS."
RL FEKS Microbiol. Lett. 78:181-196(1992).
CC -!- FUNCTION: ACTS AS A SCAFFOLDING PROTEIN IN THE CELLULOSE. IT
PROMOTES BINDING OF CELLULOSE TO THE CATALYTIC DOMAINS OF THE
CELLULOYTIC ENZYMES PROBABLY THROUGH THE BINDING OF THE NINE
REPEATED DOMAINS WITH THE DUPLICATED SEGMENT OF 24 AMINO ACIDS
PRESENT IN CATALYTIC SUBUNITS OF THE CELLULOSE.
CC -!- SUBCELLULAR LOCATION: CELL SURFACE.
CC -!- DOMAIN: THE COHESIN DOMAINS BIND TO THE DOCKERIN DOMAIN BORN BY
THE CATALYTIC COMPONENTS OF THE CELLULOSE.
```

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CC CC -1- SIMILARITY: Contains at least 3 cohesin domains.
CC CC -1- SIMILARITY: Contains 2 dockerin domains.
CC CC -----
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CC CC -----
CC CC EMBL: X68233; CAA48312.1; -.
CC CC HSSP: G06851; INSC.
CC CC DR DR
CC CC InterPro: IPR001956; CBD_3.
CC CC InterPro: IPR002102; Cohesin.
CC CC InterPro: IPR002105; Dockerin_1.
CC CC InterPro: IPR002048; EF-hand.
CC CC Pfam: PF00942; CEX_3; 1.
CC CC Pfam: PF00963; Cohesin; 3.
CC CC Pfam: PF00404; Dockerin_1; 2.
CC CC ProDom: PD001947; CBD_3_1.
CC CC PROSITE: PS00018; EF_HAND; UNKNOWN_1.
CC CC PROSITE: PS00448; CLOS_CELLULOSE_RPT; 2.
CC CC Cellulose degradation; Cell wall; Glycoprotein; Repeat.
CC CC NON TER 1
CC CC FT DOMAIN 1 80
CC CC FT DOMAIN 81 93
CC CC FT DOMAIN 94 240
CC CC FT DOMAIN 241 272
CC CC FT DOMAIN 273 439
CC CC FT DOMAIN 440 461
CC CC FT DOMAIN 462 607
CC CC FT DOMAIN 716 733
CC CC FT DOMAIN 743 746
CC CC FT DOMAIN 772 AA; 8249; MW; SF06D55E094FE10 CRC64;
CC CC SEQUENCE

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Query Match: 90.9%; Score 30; DB 1; Length 772;

Best Local Similarity 85.7%; Pred. No. 14;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLKISR 7

DB 672 YTLKISR 678

RESULT 13

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ID CIPA_CLOTH STANDARD; PRT: 1853 AA.
AC Q06851;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellulosomal scaffolding protein A precursor (Cellulosomal
DE glycoprotein S1/S1) (Cellulose integrating protein A) (Cohesin).
DE CIPA.
GN Clostridium thermocellum.
OS Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=515;
'11_TaxID=515;
RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-40 AND 42-43.
RC STRAIN=ATCC 27405 / DSM 1237;
RC MEDLINE=93302508; PubMed=9316063;
RA Gerndross U.T., Romaniec M.P.M., Kobayashi T., Huskisson N.S.,
RA Demain A.L.;
RT "Sequencing of a clostridium thermocellum gene (cipa) encoding the
RT cellulosomal SU-protein reveals an unusual degree of internal
RT homology.";
RL Mol. Microbiol. 8:325-334(1993).
RN [2]
RP SEQUENCE OF 1820-1853 FROM N.A.
RX MEDLINE=93205931; PubMed=8458832;
RA Fujino T., Beguin P., Aubert J.-P.;

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RT "Organization of a Clostridium thermocellum gene cluster encoding the
RT cellulosomal scaffolding protein cipa and a protein possibly involved
RT in attachment of the cellulose to the cell surface.";
RL G. Bacteriol. 175:1891-1899(1993).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 184-321.
RX MEDLINE=97238934; PubMed=9083107;
RA Shimizu L.J.W., Bayer E.A., Morag E., Lamed R., Yaron S., Shoham Y.,
RA Frolow F.;
RA Steitz T.A.;
RT "Crystal structure of a bacterial family-III cellulose-binding
RT domain: a general mechanism for attachment to cellulose.";
RL EMBO J. 15:5739-5751(1996).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 1213-1361.
RX MEDLINE=98022914; PubMed=9402065;
RA Tavares G.A., Beguin P., Alzari P.M.;
RT "The crystal structure of a type I cohesin domain at 1.7-A
RT resolution.";
RL J. Mol. Biol. 273:701-713(1997).
CC -1- FUNCTION: ACTS AS A SCAFFOLDING PROTEIN IN THE CELLULOSE. IT
CC PROMOTES BINDING OF CELLULOSE TO THE CATALYTIC DOMAINS OF THE
CC CELLULOLYTIC ENZYMES.
CC -1- SUBCELLULAR LOCATION: CELL SURFACE.
CC -1- DOMAIN: THE COHESIN DOMAINS BIND TO THE DOCKERIN DOMAIN BORN BY
CC THE CATALYTIC COMPONENTS OF THE CELLULOSE.
CC -1- SIMILARITY: Contains 9 cohesin domains.
CC -1- SIMILARITY: Contains 2 dockerin domains.
CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL: L08665; -; NOT ANNOTATED_CDS.
CC CC EMBL: X67506; CAA47870.1; -.
CC CC PIR: S36859; S36859.
CC CC PDB: 1AKU; 23-JUL-97.
CC CC PDB: 1AOK; 08-JUL-98.
CC CC PDB: 1NBC; 26-SEP-97.
CC CC InterPro: IPR001956; CBD_3.
CC CC InterPro: IPR002102; Cohesin.
CC CC InterPro: IPR002105; Dockerin_1.
CC CC InterPro: IPR002048; EF-hand.
CC CC Pfam: PF00942; CBD_3; 1.
CC CC Pfam: PF00963; Cohesin; 9.
CC CC Pfam: PF00404; Dockerin_1; 2.
CC CC ProDom: PD001947; CBD_3_1.
CC CC PROSITE: PS00018; EF_HAND; UNKNOWN_1.
CC CC PROSITE: PS00448; CLOS_CELLULOSE_RPT; 2.
CC CC Cellulose degradation; Cell wall; Glycoprotein; Repeat; Signal;
CC CC 3D-structure.
CC CC SIGNAL 1 28
CC CC CHAIN 29 1853 CELLULOSONAL SCAFFOLDING PROTEIN A.
CC CC COHESIN 1.
CC CC COHESIN 2.
CC CC LINKER (PRO/THR-RICH).
CC CC CELLULOSE-BINDING (BY SIMILARITY).
CC CC LINKER (PRO/THR-RICH).
CC CC COHESIN 3.
CC CC COHESIN 4.
CC CC COHESIN 5.
CC CC COHESIN 6.

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101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 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1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 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1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 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DE 15-JUL-1999 (Rel. 38, Last annotation update):
DE Ig kappa chain V-1: region MCP 51:
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN 11;
RP SEQUENCE.
RX MEDLINE=81052016; PubMed=6776396;
RA Appella E.;
RT "Amino acid sequence of the light chain variable region of M μ 1, a
RT phosphorylcholine-binding murine myeloma protein."
RJ Mol. Immunol. 17:711-718(1980).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR: A01910; KVM51.
DR HSSP: P80362; LWTL.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003086; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS00835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT 24 39 FRAMEWORK-1.
FT 40 54 COMPLEMENTARITY-DETERMINING-1.
FT 55 61 FRAMEWORK-2.
FT 62 93 COMPLEMENTARITY-DETERMINING-2.
FT 94 102 FRAMEWORK-3.
FT 103 112 COMPLEMENTARITY-DETERMINING-3.
FT 113 113 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC42A2BC3450 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 113;
Best Local Similarity 55.7%; Pred. NC. 3.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT:KISR 7
DB 76 FT:KISR 82

Search completed: October 4, 2003, 12:22:38
Job time : 12.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw mode:

Run on: October 4, 2003, 12:17:13 : Search time 49.6667 Seconds
(without alignments)
36.370 Million cell updates/sec

Title: US-09-712-819C-6

Perfect score: 33

Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 330525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREXBL23:
1: sp.archaea:
2: sp.bacteria:
3: sp.fungi:
4: sp.human:
5: sp.invertebrate:
6: sp.mammal:
7: sp.mhc:
8: sp.organelle:
9: sp.phage:
10: sp.plant:
11: sp.rodent:
12: sp.virus:
13: sp.vertebrate:
14: sp.unclassified:
15: sp.virus:
16: sp.bacterioph:
17: sp.archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	33	100.0	104	1	Q9JL82
2	33	100.0	114	4	Q9UL80
3	33	100.0	149	1	Q8K122
4	33	100.0	238	1	Q8VC16
5	33	100.0	238	1	Q9NM37
6	33	100.0	239	1	Q8VC55
7	33	100.0	239	1	Q8K0F8
8	30	90.9	239	4	Q8NEK0
9	30	90.9	239	4	Q8TCD0
10	30	90.9	548	4	Q8WJV3
11	30	90.9	638	2	Q46453
12	30	90.9	764	5	Q8IKT5
13	30	90.9	3848	5	Q76737
14	28	84.8	31	2	Q94AX:
15	28	84.8	80	2	Q9FAA7
16	28	84.8	80	2	Q9FDR9

17	28	84.8	83	16	Q8NRS2
18	28	84.8	118	16	Q9V556
19	28	84.8	285	16	Q9RAY8
20	28	84.8	303	4	Q8WGN9
21	28	84.8	310	1	Q9CU48
22	28	84.8	327	5	Q9Y315
23	28	84.8	346	1	Q9CU16
24	28	84.8	347	10	Q93XF8
25	28	84.8	389	16	Q25171
26	28	84.8	389	16	Q9ZKGB
27	28	84.8	399	2	Q56257
28	28	84.8	449	5	Q9VC17
29	28	84.8	477	5	Q9TZG7
30	28	84.8	546	4	Q9NW40
31	28	84.8	564	16	Q99YF8
32	28	84.8	733	16	Q926C7
33	28	84.8	802	16	Q8CCH7
34	28	84.8	943	2	Q52149
35	28	84.8	980	10	Q949G3
36	28	84.8	1015	10	Q945G9
37	28	84.8	1490	5	Q9TX96
38	27	81.8	51	17	Q973A6
39	27	81.8	84	16	Q8DL27
40	27	81.8	109	4	Q9UL86
41	27	81.8	109	4	Q9UL78
42	27	81.8	147	3	Q88915
43	27	81.8	159	16	Q8Y759
44	27	81.8	171	10	Q9C8P6
45	27	81.8	204	16	Q9KM12

ALIGNMENTS

RESULT 1

Q9UL82

ID Q9UL82 PRELIMINARY; PRT: 134 AA.

AC Q9UL82; Q1-OCT-2003 (TRENBLrel. 15, Created)

DI Q1-OCT-2003 (TRENBLrel. 15, Last sequence update)

DI Q1-MAR-2003 (TRENBLrel. 23, Last annotation update)

DE Anti-myosin immunoglobulin light chain variable region (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

FN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BAUB/C;

RX MEDLINE=20448942; PubMed=10992488;

RA Maikael S., Liao L., Cunningham M.W., Diamond R.;

RT "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin.";

RL Infect. Immun. 68:5803-5808 (2000).

DR EMBL; AF206024; AAF69322.1; -

DR HSSP; P01607; IREI.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT NON_TER 1

FT NON_TER 104 104

SQ SEQUENCE 104 AA; 11360 MW; 5DA83BFD5F0AA1AE CRC64;

Query Match 100.0%; Score 33; DB 1; Length 104;

Best Local Similarity 100.0%; Pred. No. 2.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7

DR Pfam: PF00047; ig; 2;
 DR SMART: SMC0406; igv; 1;
 DR PROSITE: PSS0935; IG_LIKE; 2;
 DR PROSITE: PS00230; IG_MHC; 1;
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26234 MW; FAGEDCA3B03871D CRC64;

Query Match 90.9%; Score 30; DE 4; Length 239;
 Best Local Similarity 85.7%; Pred. No. 29;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
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 Db 96 FTLKISR 102

RESULT 10
 ID Q8WUV3 PRELIMINARY; PRT; 548 AA.
 AC Q8WUV3;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Hypothetical protein (fragment).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RZ SEQUENCE FROM N.A.
 RC T-SSUE=MUSC;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.
 DR EMBL: BCC19339; AAH19339.1; -;
 DR InterPro: IPR020051; SAV_bind.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 548 AA; 61967 MW; 1:FA3F52B1C5F56 CRC64;

Query Match 90.9%; Score 30; DB 4; Length 548;
 Best Local Similarity 85.7%; Pred. No. 62;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
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 Db 455 FTLKISR 461

RESULT 11
 ID Q46453 PRELIMINARY; PRT; 638 AA.
 AC Q46453;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE CtpA protein (fragment).
 DE CtpA.
 GN Clostridium thermocellum.
 OS Clostridium thermocellum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=515;
 RN [1]
 RZ SEQUENCE FROM N.A.
 RC Fujino T., Begun P., Aubert J.P.;
 RA "Cloning of a Clostridium thermocellum DNA fragment encoding
 RT polypeptides that bind the catalytic components of the cellulosome.";
 RL FEMS Microbiol. Lett. 94:165-170(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92394466; PubMed=1521765;
 RA Fujino T., Begun P., Aubert J.P.;
 RT "Cloning of a Clostridium thermocellum DNA fragment encoding
 RT polypeptides that bind the catalytic components of the cellulosome.";

REMS Microbiol. Lett. 94:165-170(1992).
 DR EMBL: X67406; CAA47806.1; -;
 DR HSP; Q6851; LACH.
 DR InterPro: IPR02102; Cohesin.
 DR InterPro: IPR02105; Dockerin_1.
 DR InterPro: IPR02048; EF-hand.
 DR Pfam: PFC0963; Cohesin; 3.
 DR Pfam: PF00404; Dockerin_1; 2.
 DR PROSITE: PS00448; CLOS_CELLULOsome_RPT; 2.
 DR PROSITE: PS00018; EF_HAND; 1.
 FT NON TER 1
 SQ SEQUENCE 638 AA; 68255 MW; 355C17E50AFCEB6 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 638;
 Best Local Similarity 85.7%; Pred. No. 72;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
 :|||:
 Db 538 YTLKISR 544

RESULT 12
 ID C8IKT5 PRELIMINARY; PRT; 764 AA.
 AC C8IKT5;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Peptidase, putative.
 DE PF14_0517.
 GN Plasmodium falciparum (isolate 3D7).
 CS Plasmodium falciparum (isolate 3D7).
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RZ SEQUENCE FROM N.A.
 RC STRAIN=3D7;
 RX MEDLINE=22255705; PubMed=12368864;
 RA Gardner M.C., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
 RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
 RA Chan M.-S., Nene V., Shallow S.C., Suh B., Peterson J., Anguoli S.,
 RA Perea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
 RA Martin D.M.A., Fairlamb A.H., Fraunholz M.C., Roos D.S., Ralph S.A.,
 RA McFadden G.I., Cummings J.M., Subramanian G.M., Xungai C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrell B.;
 RT "Genome sequence of the human malaria parasite Plasmodium
 RT falciparum".
 RL Nature 419:498-511(2002).
 DR EMBL: AE014824; AAN37130.1; -;
 SQ SEQUENCE 764 AA; 88502 MW; 8BD974E0FB2BC34C CRC64;

Query Match 90.9%; Score 30; DB 5; Length 764;
 Best Local Similarity 85.7%; Pred. No. 86;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
 :|||:
 Db 199 FTLKISR 205

RESULT 13
 ID O76737 PRELIMINARY; PRT; 3648 AA.
 AC O76737;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE TIPC.
 DE TIPC.
 OS Dictyostelium discoideum (Slime mold); Dictyosteliota;
 OC Eukaryota; Mycetozoa; Dictyosteliota;

OX NCBI_TaxID=44689;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=AX4;
RX MEDLINE=99331084; PubMed=13402673;
RA Stege J.T., Laub M.F., Loomis W.F.;
RT tip genes act in parallel pathways of early Dictyostelium
development.";
RL Genet. 25:64-77(1999).
DR EMBL; AF079445; AAC31916.1;
SQ SEQUENCE 3848 AA; 440033 MW; 65B671566F7AE534 CRC64;

Query Match 90.9%; Score 30; DB 5; Length 3848;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
Db 886 FTLKISR 892

RESULT 14
Q9FAA7 PRELIMINARY; PRT; 80 AA.
ID Q9FAA7
AC Q9FAA7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE Hemolysin (Fragment).
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Treponemata.
OC NCBI_TaxID=158;
RN [1]
RP SEQUENCE.
RX MEDLINE=94376628; PubMed=6030078;
RA Chu L., Holt S.C.;
RT "Purification and Characterization of a 45 kDa hemolysin from
Treponema denticola ATCC 35404.";
RL Microb. Pathog. 16:197-212(1994).
SQ SEQUENCE 31 AA; 3650 MW; 054650355C8F24C4 CRC64;

Query Match 84.8%; Score 28; DB 2; Length 31;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FTLKISR 7
Db 5 FTLKISR 11

RESULT 15
Q9FAA7 PRELIMINARY; PRT; 80 AA.
ID Q9FAA7
AC Q9FAA7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Atp1 protein.
GN ATP1.
OS Brevibacterium flavum.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OC NCBI_TaxID=92706;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC14067;
RA Sekine H., Tomita F., Yokota A.;
RT "Nucleotide sequence of atp operon of Brevibacterium flavum.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB048368; BAB13353.1;
SQ SEQUENCE 80 AA; 9339 MW; 72CD0E33367E4B33 CRC64;

Query Match 84.8%; Score 28; DB 2; Length 80;

Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 FTLKISR 6
Db 36 FTLKISR 41
Search completed: October 4, 2003, 12:25:13
Job time : 51.6667 secs

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: October 4, 2003, 12:09:26 ; Search time 60.3333 Seconds
(without alignments)
18.416 Million cell updates/sec

Title: US-09-712-819c-6

Perfect score: 33
Sequence: - FTKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 15872573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : A_Geneseq_100000000
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2: /SIDSI/gcgdataa/geneseq/geneseq-emb1/AA1981.DAT:
3: /SIDSI/gcgdataa/geneseq/geneseq-emb1/AA1982.DAT:
4: /SIDSI/gcgdataa/geneseq/geneseq-emb1/AA1983.DAT:
5: /SIDSI/gcgdataa/geneseq/geneseq-emb1/AA1984.DAT:
6: /SIDSI/gcgdataa/geneseq/geneseq-emb1/AA1985.DAT:
7: /SIDSI/gcgdataa/geneseq/geneseq-emb1/AA1986.DAT:
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19: /SIDSI/gcgdataa/geneseq/geneseq-emb1/AA1998.DAT:
20: /SIDSI/gcgdataa/geneseq/geneseq-emb1/AA1999.DAT:
21: /SIDSI/gcgdataa/geneseq/geneseq-emb1/AA2000.DAT:
22: /SIDSI/gcgdataa/geneseq/geneseq-emb1/AA2001.DAT:
23: /SIDSI/gcgdataa/geneseq/geneseq-emb1/AA2002.DAT:
24: /SIDSI/gcgdataa/geneseq/geneseq-emb1/AA2003.DAT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	32	19	AAW79207 Framework 3 region
2	33	100.0	32	22	AB86295 Murine derived ant
3	33	100.0	32	23	ABP62672 Human immunopeptid
4	33	100.0	32	23	ABP62674 Human immunopeptid
5	33	100.0	32	23	AAJ70400 Human light chain
6	33	100.0	32	23	AAJ70440 Mouse light chain
7	33	100.0	50	23	ABG30477 Human anti-CD40 mo
8	33	100.0	50	23	ABG30478 Human anti-CD40 mo
9	33	100.0	50	23	ABG30479 Human anti-CD40 mo

Homologous sequenc
Mouse derived high
Hypercalcaemia age
Partial peptide fr
OF7K.7 VK-2 L chain
VK005 VK region.
Antibody variable
Murine ID9 antibod
Mouse germline kap
Mouse germline kap
Mouse germline kap
Mouse germline kap
Mouse germline kap
Mouse germline kap
Mouse germline kap
Humanised antibody
Mucin 1 (MUC-1) bl
Antibody library r
Light chain variab
Anti-DNA antibody
Human monoclonal a
Human liver peptid
Peptide #10995 enc
Protein #8450 enc
Human brain expres
Human bone marrow
Peptide #7605 enc
Peptide #11419 enc
Human peptide enco
Human lamada light
Human kappa light
TR1.6 antibody lig
Fv region SC100 an
Fv region SC100 an

ALIGNMENTS

RESULT 1
AAW79207
ID AAW79207 standard; Protein: 32 AA.
AC AAW79207;
XX
XX
CT 21-DEC-1998 (first entry)
XX
DE Framework 3 region of human V kappa gene HUM5400.
XX

Monoclonal antibody; Mab; LO-CD2a; humanised antibody; CD2 antigen;
human lymphocyte; immune response; chimeric; graft-versus-host disease;
T-cell; transplant rejection; autoimmune disease; HUM5400.

OS Homo sapiens.

XX US5817311-A.

XX C6-OCT-1998.

XX 07-JUN-1995; 95US-0472281.

XX 07-JUN-1995; 95US-0472281.

XX 05-MAR-1993; 93US-0027008.

XX 09-SEP-1993; 93US-0119032.

XX 29-MAR-1995; 95US-0407009.

(UYLO-) UNIV CATHOLIQUE LOUWAIN.

XX Bazin H, Latimne D;

XX WPI; 1998-556337/47.

XX Inhibition of T-cell mediated immune response with anti-CD2
PT monoclonal antibody LO-CD2a used for preventing transplant
PT rejection or for treating graft-versus-host disease or auto-immune
PT diseases
XX
XX Example 7; Columns 33-34; 96pp; English.
XX This represents the amino acid sequence of the framework 3 region of
CC human V kappa gene HUM400. This is used to construct a humanised antibody
CC LO-CD2a. The invention relates to the use of the monoclonal antibody
CC (MAb) LO-CD2a or a humanised or a chimeric version of the LO-CD2a
CC antibody for the inhibition of a T-cell mediated immune response in a
CC patient. The MAb LO-CD2a (produced by hybridoma cell line M0C HS 14423)
CC can bind to an epitope on the CD2 antigen of the human lymphocytes. The
CC T-cell mediated immune response in a patient can be inhibited by
CC administering the MAb LO-CD2a or an antibody that binds to the same
CC human lymphocyte epitope as LO-CD2a. The method is used for preventing
CC transplant rejection or for treating graft-versus-host disease or for
CC treating autoimmune diseases.
XX
XX Sequence 32 AA;
SQ
Query Match 100.0%; Score 33; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
DB 15 FTLKISR 21
RESULT 2
AAB86295 ID AAB86295 standard; peptide; 32 AA.
XX
XX AAB86295;
XX
XX 13-SEP-2001 (first entry)
XX
XX Murine derived antibody Wue-1 light chain variable region FW-3.
DE
XX Antibody; Wue-1; variable region; light chain; heavy chain; antitumor;
XX immunomodulatory; cognate antigen identification; autoimmune disease;
XX tumor; multiple myeloma; lymphoma; plasmacytoma; FW-3.
XX
XX Mus sp.
XX
XX DE-9962583-A1.
XX
XX 28-JUN-2001.
XX
XX 23-DEC-1999; 93DE-1062583.
XX
XX 23-DEC-1999; 93DE-1062583.
XX
XX (MUEL/) MUELLER-HERVELINK H K.
XX (GRE/) GREINER A.
XX
XX Mueller-Hermelink HK, Greiner A;
XX
XX WPI; 2001-426596/46.
XX
XX New antibodies specific for plasma cells, useful for treatment and
XX diagnosis of autoimmune diseases and plasma cell tumors .
XX
XX Claim 1; Page 10; 18pp; German.
XX This invention describes novel antibodies (Ab) in which the variable
CC region (VR) of at least one chain and/or the VR of at least one heavy
CC chain includes at least one of 7 specified sequences, or fragments of
CC these sequences, or contain at least one light chain and/or heavy
CC chain encoded by specific nucleic acid sequences (I) and (II).

CC reproduced, or their fragments. The products of the invention have
CC antitumor and immunomodulatory activity. Ab, or other antibodies that
CC recognize the same antigen, are used: (i) to identify cognate antigens;
CC (ii) for specific labeling of plasma cells (PC), for identification or
CC separation, e.g. in an extracorporeal system; (iii) for generating
CC additional antibodies able to label PC; and (iv) for treating autoimmune
CC diseases and/or tumors, e.g. multiple myeloma, lymphoma and/or
CC plasmacytoma. Ab are specific for mature PC, i.e. they do not recognize
CC precursor stages, even though these precursors are used as immunogens. As
CC therapeutic agents, they should show fewer side effects than conventional
CC chemotherapeutic agents. This sequence represents the Wue-1 antibody
CC variable region light chain FW-3 fragment described in the method of the
CC invention.
XX
XX Sequence 32 AA;
SQ
Query Match 100.0%; Score 33; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
DB 15 FTLKISR 21
RESULT 3
AAB62672 ID AAB62672 standard; Peptide; 32 AA.
XX
XX AAB62672;
XX
XX 1C-OCT-2002 (first entry)
XX
XX Human immunopeptide to HCV E2 glycoprotein framework sequence #130.
DE
XX Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
XX nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
XX NS3 protein; viral infection.
XX
XX Homo sapiens.
XX
XX MO20259340-A1.
XX
XX 01-AUG-2002.
XX
XX 25-JAN-2002; 2002WO-US03303.
XX
XX 26-JAN-2001; 2001US-264451P.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Maruyama T, Jones IV, Burton DR, Fox RI;
XX
XX WPI; 2002-599801/64.
XX
XX New human immunopolypeptide with binding specificity for certain
XX envelope glycoproteins and nonstructural proteins of hepatitis C virus
XX (HCV), for diagnosing or treating patients having or suspected of
XX having HCV infection .
XX
XX Claim 4; Fig 17; 308pp; English.
XX
XX The present invention relates to human immunopolypeptides, produced by a
XX phage transacted cell library. The present sequence is one such
XX immunopolypeptide. The immunopolypeptides have binding specificity for
XX envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
XX virus (HCV). E2 glycoprotein is believed to be responsible for target
XX cell binding and contains neutralising epitopes, while NS3 is thought to
XX be involved in the replication of HCV. The immunopolypeptides are useful
XX for diagnosing and treating a patient having or suspected to be having
XX HCV infection.
XX
XX Sequence 32 AA;

Query Match 100.0%; Score 33; DB 23; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
 15 FTLKISR 21

DE ABP62674
 AC
 ABP62674;

DT 10-OCT-2002 (first entry)

DE Human immunoprotein to HCV E2 glycoprotein; framework sequence #182.

DE Virucide; human; immunoprotein; immunoprotein; envelope glycoprotein;
 nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
 NS3 protein; viral infection.

OS Homo sapiens.

XX WO200259340-A1.

XX 01-AUG-2002.

XX 25-JAN-2002; 2002WO-US02303.

XX 26-JAN-2001; 2001US-264431P.

XX (SCRI) SCRI:PPS RES INST.

XX Maruyama T, Jones IM, Burton DP, Fox RI;
 WPI; 2002-599801/64.

XX New human immunoprotein with binding specificity for certain
 envelope glycoproteins and nonstructural proteins of hepatitis C virus
 (HCV), for diagnosing or treating patients having or suspected of
 having HCV infection.

XX Claim 4; Fig 17; 308pp; English.

XX The present invention relates to human immunoproteins, produced by a
 phage transfect cell library. The present sequence is one such
 immunoprotein. The immunoproteins have binding specificity for
 envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
 virus (HCV). E2 glycoprotein is believed to be responsible for target
 cell binding and contains neutralising epitopes, while NS3 is thought to
 be involved in the replication of HCV. The immunoproteins are useful
 for diagnosing and treating a patient having or suspected to be having
 HCV infection.

XX Sequence 32 AA;

Query Match 100.0%; Score 33; DB 23; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
 15 FTLKISR 21

DE AAU70400
 AC
 AAU70400;

DE AAU70400 standard; Peptide; 32 AA.

XX 14-FEB-2002 (first entry)

XX Human light chain immunoglobulin; framework region 3 #2.

XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 complementarity determining region; framework region; -GBP;
 transgenic plant; immunoglobulin binding protein array;
 IGM; IGG; IGA; IGD; IGE; IGY; IGM; kappa; lambda; CHSP.

OS Homo sapiens.

XX WO200183806-A1.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14349.

XX 02-MAY-2000; 2000US-0563222.

XX (EPIC-) EPICYTE PHARM INC.

XX Hiatt AC, Hein MB;

XX WPI; 2002-055482/07.

XX Preparing immunoglobulin binding protein array in plant cells by
 transforming the cells with different polynucleotides encoding binding
 protein polypeptides specific to ligand, selecting plant cells for
 preparing array.

XX Disclosure; Fig 1A; 129pp; English.

XX The invention relates to transforming a population of cells (e.g. plant
 cells), comprising using a library of two different polynucleotides
 encoding different immunoglobulin binding protein (IGBP) polypeptides
 that specifically bind to a ligand or form one or more disulfide bonds
 with polypeptides in transfected cells, to generate an IGBP that
 binds to a ligand, and transformed cells. At least one IGBP that
 preparing an IGBP array in plant cells. At least one peptide sequence has
 at least 75% sequence identity to a framework region (FR) of a native
 IGP, IGG, IGA, IGD, IGE, IGY, kappa or lambda immunoglobulin molecule.
 The method is useful for preparing an immunoglobulin binding protein
 array, preferably heavy chain binding protein (CHBP) array in eukaryotic
 cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)
 or other eukaryotic cells (e.g. insect cells or mammalian cells). The
 CHBP is useful for discovery of e.g. screening assays of IGbps having
 desired characteristics. The present sequence is a mammalian
 immunoglobulin derived peptide that may be incorporated into an IGBP of
 the invention.

XX Sequence 32 AA;

Query Match 100.0%; Score 33; DB 23; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
 15 FTLKISR 21

DE AAU70440
 AC
 AAU70440;

DE AAU70440 standard; Peptide; 32 AA.

XX 14-FEB-2002 (first entry)

XX Mouse light chain immunoglobulin framework region 3 #2.

XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;

KW complementarity determining region; framework region; IgBP;
 KW transgenic plant; immunoglobulin binding protein array;
 KW IGM; Igg; IGA; IGD; IGE; IGY; IGM; kappa; lambda; CHBP.

XX Mus musculus.

OS WO200183806-A1.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14349.

XX 02-MAY-2000; 2000US-0563222.

XX (EPIC-) EPICYTE PHARM. INC.

XX Hiatt AC, Hein MB;

XX WPI; 2002-055482/07.

XX Preparing immunoglobulin binding protein array in plant cells by
 PT transforming the cells with different polynucleotides encoding binding
 PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array

XX Disclosure; Fig 1A; 129pp; English.

XX The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IgBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IgBP that
 CC binds to a ligand, and transformed plant cells are selected, and
 CC preparing an IgBP array in plant cells. At least one peptide sequence has
 CC at least 75% sequence identity to a framework region (FR) of a native
 CC IGM, IGG, IGA, IGD, IGE, IGY, kappa or lambda immunoglobulin molecule.
 CC The method is useful for preparing an immunoglobulin binding protein
 CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic
 CC cells especially plant cells (e.g. Agrobacterium tumefaciens or maize;
 CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The
 CC CHBP is useful for discovery of e.g. screening assays of IgBPs having
 CC desired characteristics. The present sequence is a mammalian
 CC immunoglobulin derived peptide that may be incorporated into an IgBP of
 CC the invention.

XX Sequence 32 AA;

Query Match 100.0%; Score 33; DB 23; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

QY 1 FTLKISR 7

DB 15 FTLKISR 21

RESULT 7

ABG30477

ID ABG30477 standard; Protein; 50 AA.

XX ABG30477;

XX 07-OCT-2002 (first entry)

XX Human anti-CD40 monoclonal antibody 5H7 light chain #2.

XX Human; light chain; CD40; autoimmune disease; multiple sclerosis;
 KW systemic lupus erythematosus; psoriasis; inflammatory bowel disease;
 KW Crohn's disease; rheumatoid arthritis; organ rejection; lymphoma;
 KW non-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein;
 KW proliferation.

XX Homo sapiens.

XX 02-OCT-2001; 2001WO-US30857.

XX WO200228904-A2.

XX 11-APR-2002.

XX 02-OCT-2001; 2001WO-US30857.

XX 02-OCT-2000; 2000US-237556P.

XX (CHIR) CHIRON CORP.

XX Chu K, Wang C, Yoshihara C, Donnelly JJ;

XX WPI; 2002-402142/43.

XX A human anti-CD40 monoclonal antibody or fragment useful for inhibiting
 PT proliferation, growth or differentiation of a normal human B cell and
 PT treating autoimmune disease such as rheumatoid arthritis or systemic
 PT lupus erythematosus.

XX Claim 1; Fig 5; 75pp; English.

XX The invention relates to a human monoclonal antibody or fragment capable
 CC of specifically binding to a human CD40 antigen (a glycoprotein expressed
 CC on the surface of human B cells), where the antibody or fragment is free
 CC of significant agonistic activity when it binds to the CD40 antigen, and
 CC the growth or differentiation is inhibited. The fragments comprise
 CC the complementarity determining region (CDR) of the light and heavy
 CC chains of the monoclonal antibodies secreted by a hybridoma consisting of
 CC 153B, 20C4, 12D9, 9F7 and 13B4. Also included are the nucleic acids
 CC encoding the antibody (or fragments). The antibodies or fragments
 CC are used for inhibiting proliferation, growth or differentiation of a
 CC normal human B cell and to inhibit antibody production by B cells.
 CC They may also be useful for treating autoimmune diseases, such as
 CC systemic lupus erythematosus, psoriasis, multiple sclerosis, inflammatory
 CC bowel disease (Crohn's disease), rheumatoid arthritis, and lymphoma
 CC (especially Non-Hodgkin's Lymphoma). The present sequence represents
 CC the antibody 5H7 (another anti-CD40 antibody) light chain.

XX Sequence 50 AA;

Query Match 100.0%; Score 33; DB 23; Length 50;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7

DB 15 FTLKISR 21

RESULT 8

ABG30478

ID ABG30478 standard; Protein; 50 AA.

XX ABG30478;

XX 07-OCT-2002 (first entry)

XX Human anti-CD40 monoclonal antibody 9F7 light chain #2.

XX Human; light chain; CD40; autoimmune disease; multiple sclerosis;
 KW systemic lupus erythematosus; psoriasis; inflammatory bowel disease;
 KW Crohn's disease; rheumatoid arthritis; organ rejection; lymphoma;
 KW non-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein;
 KW proliferation.

XX Homo sapiens.

XX WO200228904-A2.

XX 11-APR-2002.

XX 02-OCT-2001; 2001WO-US30857.

```

XX 02-OCT-2000; 2000US-237556P.
XX (CHIR ) CHIRON CORP.
XX Chu K, Wang C, Yoshihara C, Donnelly JJ;
XX WPI; 2002-402142/43.
XX
XX A human anti-CD40 monoclonal antibody or fragment useful for inhibiting
XX proliferation, growth or differentiation of a normal human B cells and
XX treating autoimmune disease such as rheumatoid arthritis or systemic
XX lupus erythematosus -
XX
XX Claim 1; Fig 5; 75pp; English.
XX
XX The invention relates to a human monoclonal antibody or fragment capable
XX of specifically binding to a human CD40 antigen (a glycoprotein expressed
XX on the surface of human B cells), where the antibody or fragment is free
XX of significant agonistic activity when it binds to the CD40 antigen, and
XX the growth or differentiation is inhibited. The fragments comprise
XX the complementarity determining region (CDR) of the light and heavy
XX chains of the monoclonal antibodies secreted by a hybridoma consisting of
XX 15B8, 20C4, 12D9, 9F7 and 13E4. Also included are the nucleic acids
XX encoding the antibody (or fragments). The antibodies or fragments
XX are used for inhibiting proliferation, growth or differentiation of a
XX normal human B cells and to inhibit antibody production by B cells.
XX They may also be useful for treating autoimmune diseases, such as
XX systemic lupus erythematosus, psoriasis, multiple sclerosis, inflammatory
XX bowel disease (Crohn's disease), rheumatoid arthritis, and lymphoma
XX (especially Non-Hodgkin's lymphoma). The present sequence represents
XX the antibody 9F7 light chain.
XX
XX Sequence 50 AA;
XX
XX Query Match 100.0%; Score 33; DB 23; Length 50;
XX Best Local Similarity 100.0%; Pred. No. 2.9; Indels 0; Gaps 0;
XX Matches 7; Conservative 0; Mismatches 0;
XX
XX 1 FTLKISR 7
XX |||||
XX 15 FTLKISR 21
XX
XX RESULT 9
XX ABG30479
XX ID ABG30479 standard; Protein; 50 AA.
XX AC
XX XX
XX XX
XX 07-OCT-2002 (first entry);
XX
XX Human anti-CD40 monoclonal antibody 1588 light chain #2.
XX
XX Human; light chain; CD40; autoimmune disease; multiple sclerosis;
XX systemic lupus erythematosus; psoriasis; inflammatory bowel disease;
XX Crohn's disease; rheumatoid arthritis; organ rejection; lymphoma;
XX non-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein;
XX proliferation.
XX
XX Homo sapiens.
XX
XX WO200228904-A2.
XX
XX 11-APR-2002.
XX
XX 02-OCT-2001; 2001WO-US30857.
XX
XX 02-OCT-2000; 2000US-237556P.
XX (CHIR ) CHIRON CORP.
XX Chu K, Wang C, Yoshihara C, Donnelly JJ;

```

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XX WPI; 2002-402142/43.
XX
XX A human anti-CD40 monoclonal antibody or fragment useful for inhibiting
XX proliferation, growth or differentiation of a normal human B cells and
XX treating autoimmune disease such as rheumatoid arthritis or systemic
XX lupus erythematosus -
XX
XX Claim 1; Fig 5; 75pp; English.
XX
XX The invention relates to a human monoclonal antibody or fragment capable
XX of specifically binding to a human CD40 antigen (a glycoprotein expressed
XX on the surface of human B cells), where the antibody or fragment is free
XX of significant agonistic activity when it binds to the CD40 antigen, and
XX the growth or differentiation is inhibited. The fragments comprise
XX the complementarity determining region (CDR) of the light and heavy
XX chains of the monoclonal antibodies secreted by a hybridoma consisting of
XX 15B8, 20C4, 12D9, 9F7 and 13E4. Also included are the nucleic acids
XX encoding the antibody (or fragments). The antibodies or fragments
XX are used for inhibiting proliferation, growth or differentiation of a
XX normal human B cells and to inhibit antibody production by B cells.
XX They may also be useful for treating autoimmune diseases, such as
XX systemic lupus erythematosus, psoriasis, multiple sclerosis, inflammatory
XX bowel disease (Crohn's disease), rheumatoid arthritis, and lymphoma
XX (especially Non-Hodgkin's lymphoma). The present sequence represents
XX the antibody 15B8 light chain.
XX
XX Sequence 50 AA;
XX
XX Query Match 100.0%; Score 33; DB 23; Length 50;
XX Best Local Similarity 100.0%; Pred. No. 2.9; Indels 0; Gaps 0;
XX Matches 7; Conservative 0; Mismatches 0;
XX
XX 1 FTLKISR 7
XX |||||
XX 15 FTLKISR 21
XX
XX RESULT 10
XX AAR92994
XX ID AAR92994 standard; Protein; 81 AA.
XX AC
XX XX
XX XX
XX 25-MAR-2003 (updated);
XX 18-MAY-1996 (first entry);
XX
XX Homologous sequences to antibody 1CR-R3 variable region light chain.
XX
XX 1CR-R3; monoclonal antibody; human; mouse; light chain; homology;
XX variable region; epidermal growth factor receptor; hybridoma;
XX framework; cloning; computer; algorithm; immunogenicity;
XX site-directed mutagenesis; T-lymphocyte epitope; tertiary structure;
XX point mutation; antibody engineering; protein engineering;
XX humanised antibody; antitumour; cancer; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 2
XX Region 4
XX Region 4
XX Region 24..25
XX Region 35..39
XX Region 46
XX Region 48
XX Region 50..51
XX Region
XX
XX /note= "Amino acid involved in tertiary structure"
XX /note= "Amino acid involved in tertiary structure"
XX /note= "Amino acids involved in tertiary structure"
XX /note= "Amino acids involved in tertiary structure"
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XX /note= "Amino acids involved in tertiary structure"

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FT Region 53
 FT /note= "Amino acid involved in tertiary structure"
 FT 71
 FT Region
 FT /note= "Amino acid involved in tertiary structure"
 XX EP699755-A2.
 XX
 PD 06-MAR-1996.
 XX
 XX 27-JUN-1995; 95EP-0201752.
 XX
 PR 30-JUN-1994; 94CY-0000080.
 XX
 PA (IMMUNO-) CENT IMMUNOLOGIA MOLECULAR.
 XX
 PI Rodriguez RP, Valladares JL, Mateo De Acosta Col Rio CX;
 XX
 DR WPI; 1996-130770/14.
 XX
 XX Identifying interspecies differences in amino acid sequence of Ig
 PT T-cell epitopes - by sequence comparison, also humanised antibodies
 PT confg. altered T-cell epitopes, retaining antigen specificity but
 PT not immunogenicity, esp. for tumour treatment
 XX
 PS Claim 14; Fig 1; 13pp; English.
 XX
 CC The sequence represents residues from a human immunoglobulin with
 CC homology to the light chain variable region from monoclonal antibody
 CC 10R-3 (AAR92993), specific for epidermal growth factor receptor,
 CC produced by a mouse hybridoma. The sequence is partial, and
 CC complementarity determining regions are omitted. The sequence is
 CC isolated by comparison of human and mouse immunoglobulins and
 CC analysis for T-lymphocyte antigenic sequences using a computer
 CC algorithm. Residues not within a complementarity determining region,
 CC canonical structure or variable zone may be modified to reduce
 CC immunogenicity in humans (e.g. in sequence AAR92995). This method,
 CC which involves the introduction of only a few point mutations into
 CC T-cell epitope coding regions, is generally applicable in humanisation
 CC of mouse antibodies. The resulting humanised antibodies may be used
 CC e.g. as antitumour agents. They retain the antigen recognition of the
 CC original antibody, but are not immunogenic in humans.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 81 AA;
 Query Match 100.0%; Score 33; DB 17; Length 8;
 Best Local Similarity 100.0%; Pred. NC. 4.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLKISR 7
 DB 53 FTLKISR 59
 RESULT 11
 AAR80082
 ID AAR80082 standard; Protein; 89 AA.
 XX
 AC AAR80082;
 XX
 XX 22-MAY-1996 (first entry);
 DE Mouse derived light chain RT3 phage antibody pattern I.
 XX
 XX Light chain; RT3; murine; catalytic antibody; bacteriophage;
 KW pattern I.
 KW Mus musculus.
 OS
 XX
 PH Key Location/Qualifiers
 FT 1.14
 FT /note= "framework region 1"
 FT 15.28
 FT Region

FT Region
 FT /note= "complementarity determining region 1"
 FT 29.42
 FT /note= "framework region 2"
 FT 43.49
 FT /note= "complementarity determining region 2"
 FT 50.82
 FT /note= "framework region 3"
 FT 83.89
 FT /note= "complementarity determining region 3
 FT N-terminal fragment"
 XX
 XX WO9527045-A1.
 XX
 PD 12-OCT-1995.
 XX
 PD 30-MAR-1994; 94WO-US03420.
 XX
 PR 30-MAR-1994; 94WO-US03420.
 XX
 PA (IGEN-) IGEN INC.
 XX
 XX Chiswell D, Darsley M, Fitzgerald K, Kenten JH;
 PI Martin MT, McGafferty J, Smith RG, Titmas RC, Williams RO;
 XX
 DR WPI; 1995-358624/46.
 DR N-PSDB; AAT04629.
 XX
 XX Production of catalytic antibodies displayed on phage by
 PT generating a gene library of antibody-derived domains and expressing
 PT it in phage vectors
 XX
 PS Disclosure; Fig 10; 13pp; English.
 XX
 CC AAT04629 encodes AAR80082 mouse derived light chain RT3 phage antibody.
 CC The DNA was used in the prepn. of catalytic antibody (CA) producing
 CC bacteriophage. The CA can be used to activate/deactivate a
 CC biological function in an animal by enhancing the rate of cleavage,
 CC or formation of a specific bond within a mol. in vivo.
 XX
 SQ Sequence 89 AA;
 Query Match 100.0%; Score 33; DB 16; Length 89;
 Best Local Similarity 100.0%; Pred. NC. 5.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLKISR 7
 DB 65 FTLKISR 71
 RESULT 12
 AAR27009
 ID AAR27009 standard; peptide; 92 AA.
 XX
 AC AAR27009;
 XX
 XX 20-MAY-1998 (first entry);
 DE Hypercalcaemia agent portion 2.
 XX
 XX Antihuman parathyroid hormone-related protein; monoclonal antibody;
 KW variable region; rodent/human chimeric MA; constant region; FTHrP.
 XX
 OS Synthetic.
 XX
 XX JP04228069-A.
 PD 18-AUG-1992.
 XX
 XX 15-MAY-1991; 91JP-C110565.
 XX
 PR 15-MAY-1990; 90JP-C124581.
 XX

PA (KANE) KANEKA CORP.
XX
DR WPI; 1992-120987/39.
XX
XX
PT Treatment and preventive agent for hypercalcaemia - cortg. one of
PT anti-human para-thyroid hormone-related protein monoclonal antibody,
PT a rodent or chimera monoclonal antibody, fused gene and cell
PT line, etc.
XX
XX
PS Disclosure; Page 13; 18pp; Japanese.
PS
XX
XX The sequences given in AAR27009-11 are fragments which were used in
CC the construction of an agent for the treating and prevention of
CC hypercalcaemia. The agent contained a portion of the anti-human
CC parathyroid hormone-related protein monoclonal antibody (anti-human
CC PTHrP MAb). The MAb was used as the active component in the agent.
CC The agent further comprises a rodent/human chimeric Vab which has a
CC rodent variable region and a human constant region and recognises
CC human PTHrP.
XX
XX
SQ Sequence 92 AA;
Query Match 100.0%; Score 33; DB 13; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
DB 68 FTLKISR 74
RESULT 13
ID AAY56670
AC AAY56670;
AC AAY56670;
DT 15-FEB-2000 (first entry)
CX
CX Partial peptide fragment of Cynomolgus V kappa cDNA clone 4-5.
CX Complementarity determining region; antibody; primate; immunogenicity;
CX Old World ape; Old World monkey; antigen-binding affinity.
CX
CX Macaca cynomolgus.
CX
CX W09955369-A1.
CX
CX 04-NOV-1999.
CX
CX 28-APR-1999; 98WO-US09131.
CX
CX 28-APR-1998; 98US-0083367.
CX (SMIK) SMITHKLINE BEECHAM CORP.
CX
CX Taylor AH;
CX
CX WPI; 2000-023265/02.
CX N-PSDB; AA239338.
CX
CX Antibodies containing donor complementarity determining regions and
PT non-human primate acceptor frameworks, having reduced immunogenicity in
PT humans -
PT
PT Claim 26; Page 101; 123pp; English.
XX
XX The invention provides an antibody (Ab) comprising donor CDRs
CC (complementarity determining regions) derived from a non-human antigen-
CC specific donor antibody, and an acceptor framework from a non-human
CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
CC specific donor antibody onto homologous Old World ape or monkey acceptor
CC frameworks. The Abs have reduced immunogenicity and are better tolerated
CC

CC in humans (because of the close similarity between the human and primate
CC proteins), but retain the full antigen-binding affinity of the donor
CC antibody.
XX
XX
SQ Sequence 93 AA;
Query Match 100.0%; Score 33; DB 21; Length 93;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
DB 76 FTLKISR 82
RESULT 14
ID AAR72067 standard; Protein; 100 AA.
XX
XX AAR72067;
AC
XX 25-MAR-2003 (updated)
DT 26-SEP-1995 (first entry)
DT
XX OF7K.7 VK-2 L chain.
DE
XX
XX Graves ophthalmopathy associated immunoglobulin protein;
XX orbital antigen; monoclonal antibody; light chain; L chain;
KW variable region; autoimmunity.
KW
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Region 23..38
FT /label= CDR1
FT Region 54..60
FT /label= CDR2
FT Region 93..100
FT /label= CDR3
XX
XX W09508336-A1.
XX
XX 30-MAR-1995.
XX
XX 22-SEP-1994; 94WO-US10756.
XX
XX 22-SEP-1993; 93US-0124469.
XX
XX (NICH) NICHOLS INST DIAGNOSTICS.
XX
XX McLachlan SX, Rapoport B;
XX
XX WPI; 1995-139383/18.
XX N-PSDB; AAQ89326.
XX
XX Graves' ophthalmopathy-associated monoclonal antibody - produced
PT by molecular cloning of immunoglobulin genes by PCR
XX
XX C-aim 4; Page 66; 94pp; English.
XX
XX L- and H-chain DNA was amplified by PCR from Graves' orbital
CC tissue and clones encoding autoimmune-associated immunoglobulin
CC fragments were obtained. 14/15 clones of L chain (kappa) regions
CC showed homology to the putative VK germline gene KL012 (given in
CC AAQ89317) and the remaining clone, OF7K.7 (AAQ89326), to the VK005
CC gene.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 100 AA;
Query Match 100.0%; Score 33; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
76 FTLKISR 82

RESULT 15
AAR72066
ID AAR72066 standard; Protein; 100 AA.
XX
AC AAR72066;
XX
DT 25-MAR-2003 (updated;
DT 26-SEP-1995 (first entry)
XX
DE VK005 VK region.
XX
KW Graves ophthalmopathy associated immunoglobulin protein;
KW orbital antigen; monoclonal antibody; light chain; L chain;
KW variable region; autoimmunity.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
Region: 23..38
FT Region: /label= CDR1
FT Region: 54..56
FT Region: /label= CDR2
FT Region: 93..100
FT Region: /label= CDR3
XX
PN WO9508336-A1.
XX
PD 30-MAR-1995.
XX
PF 22-SEP-1994; 94WO-US10756.
XX
PR 22-SEP-1993; 93US-0124469.
XX
PA (NICH-) NICHOLS INST DIAGNOSTICS.
XX
PI McLachlan SM, Rapoport B;
XX
DR WPI; 1995-139383/16.
DR N-PSDB; AAQ89325.
XX
PT Graves' ophthalmopathy-associated monoclonal antibody - produced
PT by molecular cloning of immunoglobulin genes by PCR
XX
PS Disclosure; Page 67; 94pp; English.
XX
CC L- and H-chain DNA was amplified by PCR from Graves' orbital
CC tissue and clones encoding autoimmune-associated immunoglobulin
CC fragments were obtained. 14/15 clones of L chain (kappa) regions
CC showed homology to the putative VK germline gene K1812 (given in
CC AAQ89317) and the remaining clone, OP7K.7 (AAQ89326), to the VK005
CC gene.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 100 AA;

Query Match 100.0%; Score 33; DS 16; Length 100;
Best Local Similarity 100.0%; Freq No 5.8;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
Db 76 FTLKISR 82

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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:25:27 : Search time 35.3333 Seconds
(without alignments)
3.3344 Million cell updates/sec

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Listing first 45 summaries

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11: /cgn2_6/ptodata/1/pubpaa/US09C_FUSCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_FUS.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_FUS.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US40_NEW_FUS.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	32	1	US-09-563-222-80
2	33	100.0	32	11	US-09-563-222-120
3	33	100.0	32	12	US-09-947-839-71
4	33	100.0	32	12	US-10-168-809-5
5	33	100.0	93	9	US-09-935-243-6
6	33	100.0	99	12	US-10-041-860-28
7	33	100.0	99	12	US-10-041-860-323
8	33	100.0	99	12	US-10-041-860-365
9	33	100.0	100	10	US-09-822-698A-19
10	33	100.0	100	10	US-09-840-459-21
11	33	100.0	100	10	US-09-840-459-22
12	33	100.0	100	10	US-09-840-459-23
13	33	100.0	100	10	US-09-840-459-24
14	33	100.0	100	10	US-09-840-459-25
15	33	100.0	100	10	US-09-840-459-26

Sequence 27, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 8, Appl
Sequence 28C, App
Sequence 321, App
Sequence 364, App
Sequence 7, Appl
Sequence 24, Appl
Sequence 75, App
Sequence 76, Appl
Sequence 77, Appl
Sequence 78, Appl
Sequence 79, Appl
Sequence 80, Appl
Sequence 81, Appl
Sequence 24, Appl
Sequence 38, Appl
Sequence 131, App
Sequence 132, App
Sequence 73, Appl
Sequence 74, Appl
Sequence 41749, A
Sequence 151, App
Sequence 48276, A
Sequence 2, Appl
Sequence 13, Appl
Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-563-222-80
; Sequence 80, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Heint, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 32
; TYPE: PR:
; ORGANISM: Homo sapien
; US-09-563-222-80

Query Match 100.0% Score 33; DB 11; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 2
US-09-563-222-120
; Sequence 120, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Heint, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE OF INVENTION: EUKARYOTIC CELLS

; SEQ ID NO 19
; LENGTH: 100
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: light chain variable region from a DPK 15 germ line
US-09-822-698A-19

Query Match 100.0%; Score 33; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
| | | | |
DB 76 FTLKISR 82

RESULT 10
US-09-840-459-23
; Sequence 21, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR FILING DATE: 1999-07-22
; PRIOR FILING DATE: 1999-07-22
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-21

Query Match 100.0%; Score 33; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
| | | | |
DB 76 FTLKISR 82

RESULT 11
US-09-840-459-22
; Sequence 22, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459

; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-22

Query Match 100.0%; Score 33; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
| | | | |
DB 76 FTLKISR 82

RESULT 12
US-09-840-459-23
; Sequence 23, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-23

Query Match 100.0%; Score 33; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
| | | | |
DB 76 FTLKISR 82

RESULT 13
US-09-840-459-24
; Sequence 24, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.

APPLICANT: Horvath, Christopher
 APPLICANT: Newman, Walter
 APPLICANT: Jones, S. Tarran
 APPLICANT: O'Brien, Siobhan H.
 APPLICANT: O'Keefe, Theresa
 TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
 TITLE OF INVENTION: METHODS OF USE THEREFOR
 FILE REFERENCE: 1855.1052-012
 CURRENT APPLICATION NUMBER: US/09/840,459
 PRIOR FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: PCT/US01/03537
 PRIOR FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: 09/497,625
 PRIOR FILING DATE: 2000-02-03
 PRIOR APPLICATION NUMBER: 09/359,193
 PRIOR FILING DATE: 1999-07-22
 PRIOR APPLICATION NUMBER: 09/121,781
 PRIOR FILING DATE: 1999-07-23
 NUMBER OF SEQ ID NOS: 107
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 24
 LENGTH: 100
 TYPE: PRT
 ORGANISM: Mus musculus
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (1)...(100)
 OTHER INFORMATION: Xaa = Any Amino Acid
 S-09-840-459-24

Query Match 100.0%; Score 33; DB 10; Length 100;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 FTLKISR 7
 |||||
 b 76 FTLKISR 82

RESULT 14
 S-09-840-459-25
 Sequence 25, Application US/09840459
 Patent No. US20020150576A1
 GENERAL INFORMATION:
 APPLICANT: Larosa, Gregory J.
 APPLICANT: Horvath, Christopher
 APPLICANT: Newman, Walter
 APPLICANT: Jones, S. Tarran
 APPLICANT: O'Brien, Siobhan H.
 APPLICANT: O'Keefe, Theresa
 TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
 TITLE OF INVENTION: METHODS OF USE THEREFOR
 FILE REFERENCE: 1855.1052-012
 CURRENT APPLICATION NUMBER: US/09/840,459
 PRIOR FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: PCT/US01/03537
 PRIOR FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: 09/497,625
 PRIOR FILING DATE: 2000-02-03
 PRIOR APPLICATION NUMBER: 09/359,193
 PRIOR FILING DATE: 1999-07-22
 PRIOR APPLICATION NUMBER: 09/121,781
 PRIOR FILING DATE: 1998-07-23
 NUMBER OF SEQ ID NOS: 107
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 25
 LENGTH: 100
 TYPE: PRT
 ORGANISM: Mus musculus
 S-09-840-459-25

Query Match 100.0%; Score 33; DB 10; Length 100;
 Best Local Similarity 100.0%; Pred. No. 5.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FTLKISR 7
 |||||
 Db 76 FTLKISR 82

RESULT 15
 US-09-840-459-26
 Sequence 26, Application US/09840459
 Patent No. US20020150576A1
 GENERAL INFORMATION:
 APPLICANT: Larosa, Gregory J.
 APPLICANT: Horvath, Christopher
 APPLICANT: Newman, Walter
 APPLICANT: Jones, S. Tarran
 APPLICANT: O'Brien, Siobhan H.
 APPLICANT: O'Keefe, Theresa
 TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
 TITLE OF INVENTION: METHODS OF USE THEREFOR
 FILE REFERENCE: 1855.1052-012
 CURRENT APPLICATION NUMBER: US/09/840,459
 PRIOR FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: PCT/US01/03537
 PRIOR FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: 09/497,625
 PRIOR FILING DATE: 2000-02-03
 PRIOR APPLICATION NUMBER: 09/359,193
 PRIOR FILING DATE: 1999-07-22
 PRIOR APPLICATION NUMBER: 09/121,781
 PRIOR FILING DATE: 1998-07-23
 NUMBER OF SEQ ID NOS: 107
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 26
 LENGTH: 100
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-840-459-26

Query Match 100.0%; Score 33; DB 10; Length 100;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
 |||||
 Db 76 FTLKISR 82

Search completed: October 4, 2003, 12:42:39
 Job time : 35.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:15:51 : Search time 17.6667 Seconds
(without alignments)
15.765 Million cell updates/sec

Title: US-09-712-819C-6

Perfect score: 33

Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/protdata/iaa/5A COVB pep:*

2: /cgn2_6/protdata/iaa/5B COVB pep:*

3: /cgn2_6/protdata/iaa/6A COVB pep:*

4: /cgn2_6/protdata/iaa/6B COVB pep:*

5: /cgn2_6/protdata/iaa/6C COVB pep:*

6: /cgn2_6/protdata/iaa/6D COVB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	32	1	US-08-477-877B-33
2	33	100.0	32	1	US-07-377-696C-71
3	33	100.0	32	1	US-08-129-930B-71
4	33	100.0	32	2	US-08-472-281A-33
5	33	100.0	32	2	US-08-477-989B-33
6	33	100.0	32	4	US-08-976-238A-71
7	33	100.0	61	1	US-08-497-312-15
8	33	100.0	104	3	US-08-881-237-37
9	33	100.0	108	1	US-08-488-113B-15
10	33	100.0	108	1	US-08-477-484B-15
11	33	100.0	108	1	US-08-107-569D-15
12	33	100.0	108	1	US-08-472-788A-15
13	33	100.0	108	2	US-08-477-531B-15
14	33	100.0	108	2	US-08-646-360-151
15	33	100.0	108	2	US-08-082-842A-15
16	33	100.0	108	2	US-08-378-939-22
17	33	100.0	108	2	US-08-378-939-28
18	33	100.0	108	2	US-08-378-939-30
19	33	100.0	108	3	US-08-839-765-15
20	33	100.0	108	3	US-09-136-389-151
21	33	100.0	108	3	US-09-613-838-151
22	33	100.0	110	1	US-08-244-626-2
23	33	100.0	111	1	US-07-942-245-29
24	33	100.0	112	1	US-08-053-171-15
25	33	100.0	112	1	US-08-053-171-16
26	33	100.0	112	1	US-08-331-398A-48
27	33	100.0	112	1	US-08-331-398A-49

28	33	100.0	112	1	US-08-331-398A-50
29	33	100.0	112	1	US-07-342-245-28
30	33	100.0	112	1	US-08-478-039-88
31	33	100.0	112	1	US-08-478-039-89
32	33	100.0	112	1	US-08-477-877B-89
33	33	100.0	112	1	US-08-477-252B-3
34	33	100.0	112	1	US-08-476-349A-88
35	33	100.0	112	1	US-08-476-349A-89
36	33	100.0	112	1	US-08-388-672A-25
37	33	100.0	112	2	US-08-475-500-18
38	33	100.0	112	2	US-08-472-281A-89
39	33	100.0	112	2	US-08-483-199-18
40	33	100.0	112	2	US-08-859-649-19
41	33	100.0	112	2	US-08-859-649-29
42	33	100.0	112	2	US-08-506-293-4
43	33	100.0	112	2	US-08-606-293-8
44	33	100.0	112	2	US-08-578-194-6
45	33	100.0	112	2	US-08-752-844-15

ALIGNMENTS

RESULT 1

US-08-477-877B-33
: Sequence 33, Application US/08477877B
: Patent No. 5730979

GENERAL INFORMATION:
: APPLICANT: Bazin, Herv

: APPLICANT: Latinne, Dominique
: TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Act:

: NUMBER OF SEQUENCES: 96

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Carella, Byrre, Bain, Gilfillan,

: ADDRESSEE: Cecchi, Stewart & Oistein

: STREET: 6 Becker Farm Road

: CITY: Roseland

: STATE: New Jersey

: COUNTRY: U.S.A.

: ZIP: 07068

: COMPUTER READABLE FORM:

: MEDIUM TYPE: 3.5 inch diskette

: COMPUTER: IBM PS/2

: OPERATING SYSTEM: MS-DOS

: SOFTWARE: WordPerfect 5.1

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/477,877E

: FILING DATE: 07-JUN-1995

: CLASSIFICATION: 424

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: 08/407,009

: FILING DATE: 29-MAR-1995

: APPLICATION NUMBER: 08/119,032

: FILING DATE: 09-SEP-1993

: APPLICATION NUMBER: 08/027,098

: FILING DATE: 05-MAR-1993

: ATTORNEY/AGENT INFORMATION:

: NAME: Olstein, Elliot M.

: REGISTRATION NUMBER: 24,025

: REFERENCE/DOCKET NUMBER: 61750-146

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 201-994-1700

: TELEFAX: 201-994-1744

: INFORMATION FOR SEQ ID NO: 33:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 32 amino acids

: TYPE: amino acid

: STRANDEDNESS:

: TOPOLOGY: linear

: MOLECULE TYPE: polypeptide

US-08-477-877B-33

Query Match

100.0%

Score 33;

DB 1;

Length 32;

Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 2
US-07-977-696C-71
; Sequence 71, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Paduan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination;
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPJAWSKI
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977.696C
; FILING DATE: 11-16-92
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRPC-005A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 748-6868
; TELEFAX: (510) 748-6688
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-977-696C-71

Query Match 100.0%; Score 33; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 3
US-08-129-9108-71
; Sequence 71, Application US/081299303
; Patent No. 584187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Paduan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and

Query Match 100.0%; Score 33; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 4
US-38-472-281A-33
; Sequence 33, Application US/08472281A
; Patent No. 5817311
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Act
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bair, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472.281A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995

APPLICATION NUMBER: 06/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 06/127,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1744
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: polypeptide

JS-08-472-281A-33

Query Match 100.0%; Score 33; DB 2; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.1; DB 2; Length 32;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NY 1 FTLKISR 7

b 15 FTLKISR 21

RESULT 5

S-08-477-989B-33

Sequence 33, Application US/08477989B

Patent No. 5951983

GENERAL INFORMATION:

APPLICANT: Bazin, Herv

APPLICANT: Latipne, Dominique

APPLICANT: Kapian, Ruth

APPLICANT: Kieber-Emmons, Thomas

APPLICANT: Postema, Christina E.

APPLICANT: White-Schart, Mary

TITLE OF INVENTION: LC-CD2a Antibody and Uses

TITLE OF INVENTION: Thereof for Inhibiting

TITLE OF INVENTION: T-Cell Activation

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carella, Byrre, Bain, Gilfillan,

ADDRESSEE: Cecchi, Stewart & Olstein

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,989B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/407,009

FILING DATE: 29-MAR-1995

APPLICATION NUMBER: 08/119,032

FILING DATE: 09-SEP-1993

APPLICATION NUMBER: 08/027,008

FILING DATE: 05-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Olstein, Elliot M.

REGISTRATION NUMBER: 24,025

REFERENCE/DOCKET NUMBER: 61750-147

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: polypeptide

US-08-477-989B-33

Query Match 100.0%; Score 33; DB 2; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.1; DB 2; Length 32;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NY 1 FTLKISR 7

DB 15 FTLKISR 21

RESULT 6

US-08-976-288A-71

Sequence 71, Application US/08976288A

Patent No. 6315997

GENERAL INFORMATION:

APPLICANT: do Couto Dr., Fernando J.R.

APPLICANT: Ceriani Dr., Roberto L.

APPLICANT: Peterson Dr., Jerry A.

APPLICANT: Padlan Dr., Eduardo A.

TITLE OF INVENTION: Analogue Peptides With Broad

TITLE OF INVENTION: Carcinoma Specificity, and Kit and

TITLE OF INVENTION: Diagnostic Vaccination and

TITLE OF INVENTION: Therapeutic Methods

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder & Poplawski

STREET: 444 South Flower St., 19th Floor

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS 5.0

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/976,288A

FILING DATE: No. 6315997ender 21, 1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/129,930

FILING DATE: September 30, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/977,696

FILING DATE: No. 6315997ender 16, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Viviana Amzel Ph.D.

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: P6639938

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 622-7700

TELEFAX: (213) 489-4210

TELEX: n.a.

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-976-288A-71

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Query Match      100.0%; Score 33; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 15 FTLKISR 21

RESULT 7
US-08-497-312-19
; Sequence 19, Application US/08497312
; Patent No. 5742120
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Method for obtaining modified
; TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine
; TITLE OF INVENTION: antibody variable domains, compositions containing them.
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
; STREET: 215 Y 15, ATAREY PLAZA
; CITY: HAVANA
; STATE:
; COUNTRY: CUBA
; ZIP: 11600
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.10 (EPO);
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/497,312
; FILING DATE: 30-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CU 88/94
; FILING DATE: 30-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BOND, LAURENCE B.
; REGISTRATION NUMBER: 30,549
; REFERENCE/DOCKET NUMBER: 2629US
; TELEPHONE: 801/532-1922
; TELEFAX: 801/531-9168
; TELEX: 388961 LPY04UT
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-497-312-19

Query Match      100.0%; Score 33; DB 1; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 53 FTLKISR 59

RESULT 8
US-08-881-037-37
; Sequence 37, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mortison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Koski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 2034421:0710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5630
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-881-037-37

Query Match      100.0%; Score 33; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 68 FTLKISR 74

RESULT 9
US-08-488-113B-151
; Sequence 151, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:

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: APPLICATION NUMBER: US 07/988,430
: FILING DATE: 09-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/901,707
: FILING DATE: 19-JUN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/787,567
: FILING DATE: 04-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: McNicholas, Janet M.
: REGISTRATION NUMBER: 32,918
: REFERENCE/DOCKET NUMBER: 1:022US07/200-70.P3.C2A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/707-8889
: TELEFAX: 312/707-9155
: TELEX: 650 388-1248
: INFORMATION FOR SEQ ID NO: 151:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 108 amino acids
: TYPE: amino acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: US-08-477-494B-151

Query Match 100.0%; Score 33; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative C; Mismatches 0; Indels 0; Gaps 0;

Cq 1 PTLKISR 7
Db 72 PTLKISR 78

RESULT 11
US-08-107-669D-15
: Sequence 15, Application US/08:07569D
: Patent No. 5766886
: GENERAL INFORMATION:
: APPLICANT: Studnicka, Gary M.
: TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
: NUMBER OF SEQUENCES: 67
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.C.L.C.
: STREET: 1100 New York Ave., N.W., Suite 600
: CITY: Washington
: STATE: D.C.
: COUNTRY: United States of America
: Z-P: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/06/107,669D
: FILING DATE: 13-AUG-1993
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US92/10936
: FILING DATE: 14-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/809,464
: FILING DATE: 13-DEC-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Michele A. Cimbala
: REGISTRATION NUMBER: 33,851
: REFERENCE/DOCKET NUMBER: 0610.10C0001/MAC
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202/371-2600
: TELEFAX: 202/371-2540
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 108 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-107-669D-15
Query Match 100.0%; Score 33; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 72 FTLKISR 78

RESULT 12
US-08-472-788A-15
; Sequence 15, Application US/08472788A
; Patent No. 5770196
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,788A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,842
; FILING DATE: 23-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.10000003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-472-788A-15
Query Match 100.0%; Score 33; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 72 FTLKISR 78

RESULT 13
US-09-477-531B-15
; Sequence 15, Application US/08477531B
; Patent No. 5821123
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.2F
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,531B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/107,653
; FILING DATE: 13-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.10000004/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-477-531B-15
Query Match 100.0%; Score 33; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 72 FTLKISR 78

RESULT 14
US-08-646-360-15
; Sequence 51, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
```

ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.C, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,360
 FILING DATE: 13-MAY-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/05340
 FILING DATE: 12-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 203-70.P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8899
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 108 amino acids
 TYPE: amino acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-082-842A-15

Query Match 100.0%; Score 33; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
 Db 72 FTLKISR 78

Search completed: October 4, 2003, 12:27:23
 Job time: 18.6667 secs

Query Match 100.0%; Score 33; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FTLKISR 7
 72 FTLKISR 78

RESULT 15
 S-08-082-842A-15
 Sequence 15, Application: US/08082842A
 Patent No. 5869619
 GENERAL INFORMATION:
 APPLICANT: Studnicka, Gary M.
 TITLE OF INVENTION: Modified Antibody Variable Domains
 NUMBER OF SEQUENCES: 89
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
 STREET: 1100 New York Ave., N.W., Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.C, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/082,842A
 FILING DATE: 23-JUN-1993

GenCore version: 5.1.6
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CM protein - protein search, using sw mode:

Run on: October 4, 2003, 12:40:52 / Search time 19.3333 Seconds
(without alignments)
34,920 Million cell updates/sec

Title: US-09-712-819c-1
Perfect score: 32
Sequence: 1 FTLTSS 7
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 36168692 residues

Total number of hits satisfying chosen parameters: 456

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 761:
1: PIR:
2: PIR:
3: PIR:
4: PIR:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	34.4	4	2 A40135	branched-chain-ami
2	11	34.4	4	2 PT0644	T-cell receptor be
3	11	34.4	5	2 B44817	34.5K structural p
4	11	34.4	5	2 D44817	35K structural pro
5	10	31.2	7	2 E30608	IG kappa chain V-I
6	9	28.1	3	3 T13892	Cytochrome-c oxid
7	9	28.1	5	2 E42164	flagellar protein
8	9	28.1	5	2 E60274	major protein ant
9	9	28.1	5	2 A37114	hypoxanthine phosph
10	9	28.1	5	2 H44917	34.5K structural p
11	9	28.1	5	2 F44817	34.5K structural p
12	9	28.1	5	2 S62237	surface protein co
13	9	28.1	6	2 A60986	N-formyl oligopept
14	9	28.1	6	2 S14153	paraspinal crystal
15	9	28.1	6	2 A43766	28K ubiquitin immu
16	9	28.1	6	2 T37263	Y protein - human
17	9	28.1	6	2 I65546	MHC H2-DJ antigen
18	9	28.1	7	2 S25256	p16 protein - Esc
19	9	28.1	7	2 A26269	sex pheromone cavi
20	9	28.1	7	2 A30812	sex pheromone cavi
21	9	28.1	7	2 PS0254	18K protein 5527 -
22	9	28.1	7	2 P06649	puliculanase EC 3
23	9	28.1	7	2 S03066	globulin IV alpha
24	8	25.0	3	3 F08222	T-cell receptor be
25	8	25.0	4	2 PT0696	T-cell receptor be
26	8	25.0	4	2 PT0645	T-cell receptor be
27	8	25.0	4	2 PT0712	T-cell receptor be
28	8	25.0	4	2 PT0698	T-cell receptor be
29	8	25.0	4	2 PT0551	T-cell receptor be

30	8	25.0	4	2 PT0697	T-cell receptor be
31	8	25.0	5	2 A60521	glycogen phosphory
32	8	25.0	5	2 I40698	biotin B - Citreoba
33	8	25.0	5	2 T39564	ribosomal protein
34	8	25.0	5	2 T39566	ribosomal protein
35	8	25.0	5	2 T39565	ribosomal protein
36	8	25.0	5	2 T10954	hypothetical prote
37	8	25.0	5	2 T50385	tyrosin light chain
38	8	25.0	5	2 PT0308	IG heavy chain CRD
39	8	25.0	5	2 PT0596	T-cell receptor be
40	8	25.0	5	2 PT0310	T-cell receptor be
41	8	25.0	5	2 PT0397	T-cell receptor be
42	8	25.0	5	2 PT0600	T-cell receptor be
43	8	25.0	5	2 PT0729	T-cell receptor be
44	8	25.0	5	2 PT0624	T-cell receptor be
45	8	25.0	5	2 PT0686	T-cell receptor be

ALIGNMENTS

RESULT 1

A40135
branched-chain-amino-acid transaminase (EC 2.6.1.42); mitochondrial - rat (fragment)
N:Alternate names: branched-chain-amino-acid aminotransferase, mitochondrial
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 30-Sep-1993
C:Accession: A40135
R:Hutson, S.M.; Wallin, R.; Hall, T.R.
submitted to the Protein Sequence Database, March 1992
A:Reference number: A40135
A:Accession: A40135
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <HUT>
C:Keywords: aminotransferase; mitochondrion

Query Match 34.4%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ISS 7
Bb 1 VSS 3

RESULT 2

PT0644
T-cell receptor beta chain V-D-J region (111-131) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0644
R:Feeney, A.J.
C:Exp. Med. 174, 115-124, 1991
A:Title: Functional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0644
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 34.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FT 2
Bb 4 FT 5

RESULT 3

B44817
 35K structural protein - Leuconostoc oenos phage P2t11-15 (fragment)
 C:Species: Leuconostoc oenos phage P2t11-15
 C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
 C:Accession: B44817
 R:Arndt, E.K.; Lonvaud, A.; Hammes, W.P.
 J. Gen. Microbiol. 137, 2135-2139, 1991
 A:Title: Lysogeny in Leuconostoc oenos.
 A:Reference number: A44817; MUID:92085033; PMID:1748869
 A:Accession: B44817
 A:Molecule type: protein
 A:Residues: 1-5 <ABE>
 A>Note: sequence extracted from NCBI backbone (NCBI:P03423)

Query Match 34.4%; Score 11; DB 2; Length 5;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LTSS 7
 DB 1 LTSS 5

RESULT 4
 B44817
 35K structural protein - Leuconostoc oenos phage P2t11-15 (fragment)
 C:Species: Leuconostoc oenos phage P2t11-15
 C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
 C:Accession: B44817
 R:Arndt, E.K.; Lonvaud, A.; Hammes, W.P.
 J. Gen. Microbiol. 137, 2135-2139, 1991
 A:Title: Lysogeny in Leuconostoc oenos.
 A:Reference number: A44817; MUID:92085033; PMID:1748869
 A:Accession: B44817
 A:Molecule type: protein
 A:Residues: 1-5 <ABE>
 A>Note: sequence extracted from NCBI backbone (NCBI:P03423)

Query Match 34.4%; Score 11; DB 2; Length 5;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LTSS 7
 DB 1 LTSS 5

RESULT 5
 E30608
 Ig kappa chain V-III region (Gag) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
 C:Accession: E30608
 R:Coni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.; Fernandez, J.; Carson, D.; Seid
 J. Immunol. 142, 3158-3163, 1989
 A:Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
 A:Reference number: A30601; MUID:89215279; PMID:2496160
 A:Accession: E30608
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <GCG>
 C:Keywords: heterotetramer; immunoglobulin

Query Match 31.2%; Score 10; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LTSS 6
 DB 4 LTSS 7

RESULT 6
 E60274
 major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
 C:Species: Mycobacterium tuberculosis
 C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
 C:Accession: E60274
 R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
 Infect. Immun. 59, 372-382, 1991
 A:Title: Isolation and partial characterization of major protein antigens in the cult
 A:Reference number: A60274; MUID:91099989; PMID:1898899
 A:Accession: E60274
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-5 <NAG>

Query Match 28.1%; Score 9; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
 DB 3 TL 4

RESULT 7
 E42364
 flagellar protein fliR - Salmonella typhimurium (fragment)
 C:Species: Salmonella typhimurium
 C:Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 30-Sep-1993
 C:Accession: E42364
 R:Vogler, A.P.; Homma, M.; Irikura, Y.M.; Macnab, R.M.
 J. Bacteriol. 173, 3564-3572, 1991
 A:Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and
 A:Reference number: A42364; MUID:91250342; PMID:1646201
 A:Accession: E42364
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-5 <VOG>
 A:Cross-references: GB:M62408

Query Match 28.1%; Score 9; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
 DB 2 TL 3

RESULT 8
 E60274
 major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
 C:Species: Mycobacterium tuberculosis
 C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
 C:Accession: E60274
 R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
 Infect. Immun. 59, 372-382, 1991
 A:Title: Isolation and partial characterization of major protein antigens in the cult
 A:Reference number: A60274; MUID:91099989; PMID:1898899
 A:Accession: E60274
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-5 <NAG>

Query Match 28.1%; Score 9; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
 DB 2 TL 3

T13892
 cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (f
 C:Species: mitochondrion Lampetra fluviatilis (river lamprey)
 C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C:Accession: T13892
 R:Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
 Mol. Biol. Evol. 14, 807-813, 1997
 A:Title: The main features of the craniate mitochondrial DNA between the NDI and the
 A:Reference number: Z17775; MUID:97398704; PMID:9234918
 A:Accession: T13892
 A>Status: preliminary; translated from GB/EMBL/PCRJ
 A:Molecule type: DNA
 A:Residues: 1-3
 A:Cross-references: EMBL:Y09528; NID:92340016; PID:G4379123
 C:Genetics:
 A:Genome: mitochondrion
 A>Note: COI
 C:Keywords: mitochondrion; oxidoreductase

Query Match 28.1%; Score 9; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
 DB 2 TL 3

Query Match 28.1%; Score 9; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
 DB 2 TL 3

RESULT 7
 E42364
 flagellar protein fliR - Salmonella typhimurium (fragment)
 C:Species: Salmonella typhimurium
 C:Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 30-Sep-1993
 C:Accession: E42364
 R:Vogler, A.P.; Homma, M.; Irikura, Y.M.; Macnab, R.M.
 J. Bacteriol. 173, 3564-3572, 1991
 A:Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and
 A:Reference number: A42364; MUID:91250342; PMID:1646201
 A:Accession: E42364
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-5 <VOG>
 A:Cross-references: GB:M62408

Query Match 28.1%; Score 9; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
 DB 3 TL 4

RESULT 8
 E60274
 major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
 C:Species: Mycobacterium tuberculosis
 C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
 C:Accession: E60274
 R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
 Infect. Immun. 59, 372-382, 1991
 A:Title: Isolation and partial characterization of major protein antigens in the cult
 A:Reference number: A60274; MUID:91099989; PMID:1898899
 A:Accession: E60274
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-5 <NAG>

Query Match 28.1%; Score 9; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
 DB 3 TL 4

Query Match 28.1%; Score 9; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
 DB 3 TL 4

RESULT 8
 E60274
 major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
 C:Species: Mycobacterium tuberculosis
 C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
 C:Accession: E60274
 R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
 Infect. Immun. 59, 372-382, 1991
 A:Title: Isolation and partial characterization of major protein antigens in the cult
 A:Reference number: A60274; MUID:91099989; PMID:1898899
 A:Accession: E60274
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-5 <NAG>

Query Match 28.1%; Score 9; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
 DB 3 TL 4

Query Match 28.1%; Score 9; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
 DB 3 TL 4

```
Db 2 YP:15
RESULT 9
A37114
C:Species: Schistosoma mansoni
C:Title: Hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (Schistosoma mansoni) (fragment)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 23-Jun-1993
C:Accession: A37114
R:Yuan, L.; Craig, S.P.; McKerrow, J.H.; Wang, C.C.
J. Biol. Chem. 265, 13528-13532, 1990
C:Title: The hypoxanthine-guanine phosphoribosyltransferase of Schistosoma mansoni. Further characterization of the gene and protein.
A:Reference number: A37114; PMID:90337955; PMID:2199439
A:Accession: A37114
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <YU>
A:Keywords: Glycosyltransferase; pentosyltransferase
Query Match 28.1%; Score 9; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 3;
QY 5 ISS 7
Db 1 MATSS 5
RESULT 10
H44817
C:Species: Leuconostoc oenos phase P32 (fragment)
C:Title: 34.5K structural protein - Leuconostoc oenos phase P32
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: H44817
R:Arndt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
C:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; PMID:92095033; PMID:1748858
A:Accession: H44817
A:Molecule type: protein
A:Residues: 1-5 <AR>
A:Note: sequence extracted from NCBI backbone (NCBI:P:70332)
Query Match 28.1%; Score 9; DB 2; Length 5;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 3;
QY 3 LTISS 7
Db 1 MATSS 5
RESULT 11
F44817
C:Species: Leuconostoc oenos phase P54 (fragment)
C:Title: 34.5K structural protein - Leuconostoc oenos phase P54
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: F44817
R:Arndt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
C:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; PMID:92095033; PMID:1748858
A:Accession: F44817
A:Molecule type: protein
A:Residues: 1-5 <AR>
A:Note: sequence extracted from NCBI backbone (NCBI:P:70335)
Query Match 28.1%; Score 9; DB 2; Length 5;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 LTISS 7
Db 1 MATSS 5
RESULT 12
S69237
C:Species: Staphylothermus marinus
C:Title: Surface protein tetra-brachion: heavy chain - Staphylothermus marinus (fragment)
C:Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
C:Accession: S69237
R:Peterson, J.; Nitsch, M.; Kuehlmoegen, B.; Golbik, P.; Lupas, A.; Kellermann, J.; Engel, J. Mol. Biol. 245, 385-401, 1995
C:Title: Tetra-brachion: a filamentous archaeobacterial surface protein assembly of unknown function.
A:Reference number: S69237; PMID:95139068; PMID:7837271
A:Accession: S69237
A:Molecule type: protein
A:Residues: 1-5 <PET>
A:Experimental source: strain Fl, DSM 3639
A:Keywords: cell wall; glycoprotein; heat-stable protein
Query Match 28.1%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TL 3
Db 2 TL 3
RESULT 13
A60986
C:Species: Escherichia coli (fragment)
C:Title: N-formyl oligopeptide - Escherichia coli
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
C:Accession: A60986
R:Broom, M.F.; Mellor, D.X.; Chadwick, V.S.
Experientia 45, 1097-1099, 1989
C:Title: Purification and amino acid sequencing of naturally occurring N-formyl-methionine.
A:Reference number: A60986; PMID:90992408; PMID:2689204
A:Accession: A60986
A:Molecule type: protein
A:Residues: 1-6 <BRO>
A:Note: This hexapeptide was the longest of several N-formyl oligopeptides reported in the literature.
C:Modified site: N-formylmethionine #status experimental
Query Match 28.1%; Score 9; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 FTL 3
Db 3 FIL 5
RESULT 14
S14159
C:Species: Bacillus thuringiensis
C:Title: Parasporal crystal protein CryIC - Bacillus thuringiensis (fragment)
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C:Accession: S14159
R:Convents, D.; Cherlet, M.; van Damme, J.; Lasters, I.; Lauwereys, M.
Eur. J. Biochem. 195, 631-635, 1991
C:Title: Two structural domains as a general fold of the toxic fragment of the Bacillus thuringiensis delta-endotoxin.
A:Reference number: S14087; PMID:91153300; PMID:1847865
A:Accession: S14159
A:Molecule type: protein
A:Residues: 1-6 <CON>
Query Match 28.1%; Score 9; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTL 3
Db 3 FIL 5
```

Qy	5	ISS	7
Dz	1	IST	3

RESJLT 15

A:Species: Coprinus cinereus
 C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #ext_change 30-Sep-1993
 C:Accession: A43766
 R:Kanda, T.; Inoue, M.; Akiyama, M.
 Biochimie 72, 355-359, 1990
 A:Title: Purification and characterization of an ubiquitin-immune-reactive protein local
 A:Reference number: A43766; MUID:91022724; PMID:169846
 A:Accession: A43766
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-6 xKAN

Query Match	28.13;	Score 3;	DS 2;	Length 6;
Best Local Similarity	100.0;	Prod. No. 2.8e.05;		
Matches	2;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0;

Qy	2	3
Qz	5	6

Search completed: October 4, 2003, 12:49:36
Job time : 21.3333 secs

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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:27:32 ; Search time 10 seconds
(without alignments)
32.919 Million cell updates/sec

Title: US-09-712-819C-1

Perfect score: 32

Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 88

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	37.5	7	1	GFRP_MOUSE
2	11	34.4	5	1	RE31_LITRU
3	11	34.4	5	1	RE31_LITRU
4	10	31.2	5	1	Si04_LITRU
5	9	28.1	7	1	CCP_ENTFA
6	9	28.1	7	1	CIA_ENTFA
7	8	25.0	5	1	ALL4_CARMA
8	8	25.0	5	1	B08_CITFR
9	8	25.0	5	1	PSK_DAUCA
10	8	25.0	6	1	LOKI_LOGMI
11	8	25.0	7	1	ALL2_CARMA
12	8	25.0	7	1	ALL3_CARMA
13	8	25.0	7	1	ALL4_CARMA
14	8	25.0	7	1	ALL5_CARMA
15	9	25.0	7	1	ALL7_CVDEO
16	9	25.0	7	1	UC24_MAIZE
17	7	21.9	4	1	E05_HUMAN
18	7	21.9	4	1	RMO1_YEAS
19	7	21.9	5	1	B0A_CITFR
20	7	21.9	6	1	UN06_GLOPA
21	6	19.8	4	1	ACH1_ACHFU
22	6	19.8	4	1	PARK_HIRME
23	6	19.8	4	1	PARK_HIRME
24	6	19.8	4	1	PFKA_ATEL
25	6	19.8	4	1	FLRN_ATEL
26	6	19.8	4	1	FLRN_ATEL
27	6	19.8	4	1	FMRF_WACNI
28	6	19.8	4	1	FYRI_ATEL
29	6	19.9	4	1	OCPI_OCTMI
30	6	19.9	5	1	E103_LITRU
31	6	19.9	5	1	PAP2_PAPMA
32	6	19.9	5	1	PAP2_PAPMA
33	6	19.8	5	1	RE11_LITRU

34 6 18.8 5 1 RE21_LITRU
35 6 18.8 5 1 SUGA_ACHDO
36 6 18.8 5 1 TPI3_CANFA
37 6 18.8 5 1 UC22_MAIZE
38 6 18.8 6 1 CIP1_MATED
39 6 19.8 6 1 CIP2_MATED
40 6 18.8 6 1 B101_LITRU
41 6 18.8 6 1 FARP_WONEX
42 6 18.8 7 1 FARP_ASCSU
43 6 18.8 7 1 FARP_HELTI
44 6 18.8 7 1 FARP_MACRS
45 6 18.8 7 1 FARP_PROCL

ALIGNMENTS

RESULT 1
GFRP_MOUSE STANDARD; PRT; 7 AA.
ID GFRP_MOUSE
AC P99025;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE GTP cyclohydrolase I feedback regulatory protein (Pis) (Fragment).
GN GCHFR OR GFRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath.; Muridae; Murinae; Mus.
CX NCBI_taxid=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RA Sanchez J.-C., Roupe V., Frutiger S., Hughes G., Yan J.X.,
RA Hoegland C., Appel R.D., Binz P.A., Hochstrasser D.F.,
RA Cowthorne M.;
RL Submitted (AUG-1998) to the SWISS-PROT data bank.
CC -!- FUNCTION: MEDIATES TETRAHYDROPTERIN INHIBITION OF GTP
CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
(BY SIMILARITY).
CC -!- SUBUNIT: Homodimer (By similarity).
DR SWISS-2DPAGE; P99025; MOUSE.
FT INTR_MET 0 0
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 806 MW; 7185835727354700 CRC64;

Query Match 37.5%; Score 12; DB 1; Length 7;
Best Local Similarity 60.0%; Pred.No. 1;e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LTISS 7
DB 3 LLIST 7

RESULT 2
RE31_LITRU STANDARD; PRT; 5 AA.
ID RE31_LITRU
AC P82072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidris 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
CX NCBI_taxid=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion.
RA Steinbörner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;

RT "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
 CC activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAE.
 KW Amphibian defense peptide; Amidation.
 FT MOD RES 5 5 AMIDATION.
 SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB1030C30 CRC64;

Query Match 34.4%; Score 11; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
 ||
 DB 4 FT 5

RESULT 3
 RE32 LITRU
 ID RE32 LITRU STANDARD; PRT; 5 AA.
 AC P82C73;
 DT 28-FEB-2003 (Rel. 41, Created);
 DT 28-FEB-2003 (Rel. 41, Last sequence update);
 DT 15-SEP-2003 (Rel. 42, Last annotation update);
 DE Rubellidin 3.2.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
 CC activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 KW Amphibian defense peptide.
 SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A0C30 CRC64;

Query Match 34.4%; Score 11; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
 ||
 DB 4 FT 5

RESULT 4
 E104 LITRU
 ID E104 LITRU STANDARD; PRT; 5 AA.
 AC P82100;
 DT 28-FEB-2003 (Rel. 41, Created);
 DT 28-FEB-2003 (Rel. 41, Last sequence update);
 DT 15-SEP-2003 (Rel. 42, Last annotation update);
 DE Electricin 4.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 KW Amphibian defense peptide; Amidation.
 FT MOD RES 5 5 AMIDATION.
 SQ SEQUENCE 5 AA; 616 MW; 61P2D1A959A0C30 CRC64;

Query Match 31.2%; Score 10; DB 1; Length 5;
 Best Local Similarity 33.3%; Pred.No. 1.3e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTI 5
 ||
 DB 2 LTV 4

RESULT 5
 CCF1 ENTFA
 ID CCF1 ENTFA STANDARD; PRT; 7 AA.
 AC P201C4;
 DT 01-FEB-1991 (Rel. 17, Created);
 DT 01-FEB-1991 (Rel. 17, Last sequence update);
 DT 01-FEB-1991 (Rel. 17, Last annotation update);
 DE Sex pheromone CCF10.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=890C813; PubMed=3139656;
 RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
 RA Adsit J.C., Dunny G.M., Suzuki A.;
 RT "Structure of CCF-0, a peptide sex pheromone which induces
 RT conjugative transfer of the Streptococcus faecalis tetracycline
 RT resistance plasmid, pCF-0.";
 RL J. Biol. Chem. 263:14574-14578(1988).
 CC -!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC REMOVIN PLASMID PCF10.
 DR PIR; A30812; A30812.
 KW Pheromone.
 SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 28.1%; Score 9; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
 ||
 DB 3 TL 4

RESULT 6
 CIA ENTFA
 ID CIA ENTFA STANDARD; PRT; 7 AA.
 AC P11932;
 DT 01-OCT-1989 (Rel. 12, Created);
 DT 01-OCT-1989 (Rel. 12, Last sequence update);
 DT 01-FEB-1991 (Rel. 17, Last annotation update);
 DE Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=87005252; PubMed=3093276;
 RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
 RA White B.A., An F.Y., Clewell D.B., Suzuki A.;

RT "Isolation and structure of the Streptococcus faecalis sex pheromone,
 RL CAM373";
 RT FEBS Lett. 206:69-72(1986);
 CC -!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
 CC -!- HARBORING FAM373.
 CC -!- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR
 CC SPECIFICITY OF PHEROMONES TO PLASMIDS.
 CC -!- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
 DR PIR: A25269; A25269.
 KW Pheromone.
 SQ SEQUENCE 7 AA; 734 MW; 75RMD725905050500 CRC64;

Query Match: 28.1%; Score 9; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3
 DB 3 FIL 5

RESULT 7

AL14_CARMA STANDARD; PRT; 5 AA.

ID AL14_CARMA
 AC P81817;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 14.
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 CC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 CX NCBI_TaxID=6759;
 [1]

SEQUENCE

RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC Neuropeptide; Amidation: Multigene family.
 KW Neuropeptide; Amidation (POTENTIAL).
 FT MOD RES 5
 SQ SEQUENCE 5 AA; 586 MW; 672879DSAB300000 CRC64;

Query Match: 25.0%; Score 6; DB 1; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3
 DB 3 FGL 5

RESULT 8

B10B_CITFR STANDARD; PRT; 5 AA.

ID B10B_CITFR
 AC P12937;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment).
 GN B10B.
 OS Citrobacter freundii.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Citrobacter.
 CX NCBI_TaxID=546;
 [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=89006280; PubMed=2971595;
 RA Shivar D., Campbell A.;
 RT "Transcriptional regulation and gene arrangement of Escherichia coli,
 R1 Citrobacter freundii and Salmonella typhimurium biotin operons.";
 RL Gene 67:203-211(1988).
 CC -!- CATALYTIC ACTIVITY: Dethiobiotin + sulfur = Biotin.
 CC -!- PATHWAY: Biotin biosynthesis; Last step.
 CC -!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
 CC FAMILY.
 CC
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 CC
 DR EMBL; M21922; -; NOT_ANNOTATED_CDS.
 DR PIR; I40698;
 KW Biotin biosynthesis; Iron-sulfur; Transferase.
 FT NON TER 5
 SQ SEQUENCE 5 AA; 532 MW; 75ASB1EDD6700000 CRC64;

Query Match: 25.0%; Score 8; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SS 7
 DB 4 SS 5

RESULT 9

PSK_DAUCA

ID PSK_DAUCA STANDARD; PRT; 5 AA.
 AC P58261;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)].
 OS Daucus carota (Carrot).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asterales; Campanulids; Apiales; Apiaceae; Daucus.
 CX NCBI_TaxID=4039;
 [1]

RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.
 RC STRAIN=cv. US-Harumakigosun;
 RX MEDLINE=20212743; PubMed=10750705;
 RA Hanaï H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
 RA Kanada H., Sakagami Y.;

RT "A secreted peptide growth factor, phytosulfokine, acting as a
 RT stimulatory factor of carrot somatic embryo formation.";
 RL Plant Cell Physiol. 41:27-32(2000).
 CC -!- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE
 CC CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOVATIC
 CC EMBRYOS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A
 CC PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.
 KW Growth factor; Sulfation.
 FT PEPTIDE 1 4 PHYTOSULFOKINE-BETA.
 FT MOD RES 3 3 SULFATION.
 FT MOD RES 3 3 SULFATION.
 SQ SEQUENCE 5 AA; 687 MW; 76C1B554B3000000 CRC64;

Query Match: 25.0%; Score 8; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 FT 2
DB 3 Y 4

RESULT 10
LOKI_LOCKI
ID LOKI_LOCKI STANDARD; PRT; 6 AA.
AC P41491;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustakinin I.
OS Locusta migratoria (migratory locust).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Orthopteroidea; Orthoptera; Casilifera; Acridomorpha;
CC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=92262851; PubMed=1585017;
RA Schoofs L., Holman G.N., Proost P., van Damme C., Hayes J.K.,
RA de Loof A.;
RA "Locustakinin, a novel myotropic peptide from Locusta migratoria,
RT isolation, primary structure and synthesis.";
RI Regul. Pept. 37:49-57(1992).
CC -!- FUNCTION: Myotropic peptide. May be important in the stimulation
CC of ion transport and inhibition of diuretic activity in Vapigian
CC tubules.
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PIR; A61049; A61048.
KW Neuropeptide; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 654 MW; 58636585B9C3C300 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SS 7
DB 3 SS 4

RESULT 11
ALL2_CARMA
ID ALL2_CARMA STANDARD; PRT; 7 AA.
AC P81807;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 2.
OS Carcinus maenas (Common shore crab) (Green crab).
CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
CC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [2]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RA "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RI Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 770 MW; 672879CDB5DBD70 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SS 7
DB 3 SS 4

RESULT 12
ALL3_CARMA
ID ALL3_CARMA STANDARD; PRT; 7 AA.
AC P81806;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 3.
OS Carcinus maenas (Common shore crab) (Green crab).
CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
CC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RA "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RI Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Multigene family.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 796 MW; 672879CDB476B70 CRC64;

Query Match 25.0%; Score 9; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PTL 3
DB 5 FGL 7

RESULT 13
ALL4_CARMA
ID ALL4_CARMA STANDARD; PRT; 7 AA.
AC P81807;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 4.
OS Carcinus maenas (Common shore crab) (Green crab).
CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
CC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RA "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RI Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Multigene family.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 782 MW; 672879CDB476AC0 CRC64;

Query Match 25.0%; Score 9; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PTL 3
DB 5 FGL 7

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Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3
Db 5 FGL 7

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 FTL 3
Db 5 FGL 7

Search completed: October 4, 2003, 12:46:00
Job time : 12 secs

RESULT 14

ALL5-CARMA
ID -ALL5-CARMA STANDARD; PRT; 7 AA.
AC P81808;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 5.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 7
SQ SEQUENCE 7 AA; 781 MW; 672879CDCB476420 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3
Db 5 FGL 7

RESULT 15

ALL7-CYDPO
ID -ALL7-CYDPO STANDARD; PRT; 7 AA.
AC P82158;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 7.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricodea; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.J., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 7
SQ SEQUENCE 7 AA; 873 MW; 672679CABB569353 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:40:19 : Search time 48 Seconds
(without alignments:
37.633 Million cell updates/sec)

Title: US-09-712-819C-1

Perfect score: 32
Sequence: 1 PTLISS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 67

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	50.0	7	2	P70804 azotobacter
2	12	37.5	7	2	O34028 sphingomona
3	11	34.4	7	2	O54248 streptomyce
4	9	28.1	7	2	O07354 synchromococ
5	9	28.1	7	10	P82445 nicotiana
6	9	28.1	7	15	Q8JF81 rumen rumur
7	8	25.0	6	10	P82181 spinacia ol
8	8	25.0	6	10	P82182 spinacia ol
9	8	25.0	7	2	P72381 nocardiala
10	7	21.9	7	2	C47029 enterobacte
11	7	21.9	7	12	Q85578 bovine heif
12	6	18.8	5	13	P83308 gallus gall
13	6	18.8	6	10	P82541 spinacia ol
14	6	18.8	7	2	O50556 actinobacil
15	6	18.8	7	2	O8KX59 enterobacte
16	6	18.8	7	4	Q15903 homo sapien

17	6	18.8	7	8	O98866 spinacia ol
18	6	18.8	7	8	O95945 saccharomyc
19	6	18.8	7	10	Q9C5B3 arabidopsis
20	6	18.8	7	11	O8K3H6 rattus norv
21	6	18.8	7	12	O8K3H6 rattus norv
22	6	18.8	7	13	C9YGL3 transmissib
23	5	15.6	5	2	C42564 fugu rubrip
24	5	15.6	7	2	P83073 bacillus ce
25	5	15.6	7	2	O6KMS3 klebsiella
26	5	15.6	7	2	C47505 escherichia
27	5	15.6	7	2	O8G112 borrelia bu
28	5	15.6	7	2	O8G104 borrelia hu
29	5	15.6	7	8	C8M5Y6 taraxacum (
30	5	15.6	7	10	P31233 lycopersico
31	5	15.6	7	11	O63669 rattus norv
32	5	15.6	7	12	O67113 influenza vi
33	5	15.6	7	15	O07624 rous sarcom
34	4	12.5	4	11	O08433 rattus sp.
35	4	12.5	7	2	O8G100 borrelia bu
36	4	12.5	7	4	Q8NH77 homo sapien
37	4	12.5	7	8	Q15897 homo sapien
38	4	12.5	7	8	P92214 amb.yopyrium
39	4	12.5	7	8	P92393 hordeum vul
40	4	12.5	7	8	P92403 lophopyrum
41	4	12.5	7	8	P92427 peridictyon
42	4	12.5	7	8	O99182 gnatholebia
43	4	12.5	7	8	P92430 aegilops ta
44	4	12.5	7	8	P92221 bromus iner
45	4	12.5	7	8	P92425 pseudoroegn
					P92381 hordeum bra

ALIGNMENTS

RESULT 1
P70804
ID P70804 PRELIMINARY; PRT; 7 AA.
AC P70804;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DB Algt protein (Fragment).
GN Algt.
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [-]
RP SEQUENCE FROM N.A.
RC STRAIN=E;
RX MEDLINE=96427318; PubMed=8830692;
RA Rehm B.H.A., Ertesvag H., Vailla S.;
RT "A new Azotobacter vinelandii: mannuronan C-5-epimerase gene (algt) is
RT part of an alg gene cluster physically organized in a manner similar
RT to that in Pseudomonas aeruginosa";
RL J. Bacteriol. 178:5884-5889(1996).
DR EMBL; X87573; CAA61230.1; -;
FT NON TER
SQ SEQUENCE 7 AA; 684 MW; 71BSA5A5A2D1AE3C CRC64;

Query Match: 50.0%; Score 16; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TISS 7
DB 2 TVSS 5

RESULT 2
C34028
ID C34028 PRELIMINARY; PRT; 7 AA.
AC O34028;

DT 01-JAN-1998 (TREMBLrel. 05, Created);
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update);
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update);
 DE Catechol-2,3-dioxygenase (Fragment);
 GN PRNE.
 OS Sphingomonas chungkingensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
 OC Sphingomonadaceae; Sphingomonas.
 OX NCBI_TaxID=56193;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DJ77;
 RA Kim Y.-C.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; C88298; AAB66311.1; -;
 KW Dioxigenase.
 FT NON TER 1
 SQ SEQUENCE 7 AA; 958 MW; 7-A452D1A699D460 CRC64;

Query Match 37.5%; Score 12; DB 2; Length 7;
 Best Local Similarity 20.0%; Pred. No. 8.3e+05;
 Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 MISS 7
 DB 3 MVTNT 7

RESULT 3

Q54248 PRELIMINARY; PRT; 7 AA.
 AC Q54248;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RplC protein (Fragment);
 GN RPLC.
 OS Streptomyces griseus.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomyces; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=111;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2-3-11;
 RA Poehling S., Piepersberg W., Wehmeier U.F.;
 RL MEDLINE=20011291; PubMed=10542330;
 RT "Analysis and regulation of the sec Y gene from Streptomyces griseus N2-3-11 and interaction of the SecY protein with the SecE protein";
 RL Biochim. Biophys. Acta 1447:298-322(1999).
 DR EMBL; X95915; CAA65160.1; -;
 FT NON TER 1
 SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2AC CRC64;

Query Match 34.4%; Score 11; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 TIT 4
 DB 2 TIT 4

RESULT 4

O07354 PRELIMINARY; PRT; 7 AA.
 AC O07354;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update);
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE NifK (Fragment).
 GN NIFK.
 OS Synethococcus sp. (strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).
 OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.

OX NCBI_TaxID=41431;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RF-1;
 RX MEDLINE=99231861; PubMed=10217509;
 RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
 RT "Organization and expression of nitrogen-fixation genes in the aerobic nitrogen-fixing unicellular cyanobacterium Synethococcus sp. strain RF-1";
 RT Microbiology 145:743-753(1999).
 DR EMBL; AF003700; AAC3193.1; -;
 FT NON TER 1
 SQ SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B03C CRC64;

Query Match 28.1%; Score 9; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FTL 3
 DB 3 FDL 5

RESULT 5

P82445 PRELIMINARY; PRT; 7 AA.
 AC P82445;
 DT 01-JUN-2000 (TREMBLrel. 14, Created)
 DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE 10 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 CC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=sv. PETIT HAVANA;
 RA Snee K.A., Benham V.A., Mitchell G.P., Robertson D., Slabas A.P.,
 RA Wojtaszek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed tobacco culture";
 RT Planta 0:0-0(2000).
 CC -!- SUBCELLULAR LOCATION: CELL WALL.
 CC -!- TISSUE SPECIFICITY: XYLEM.
 KW Cell wall.
 FT NON TER 7
 SQ SEQUENCE 7 AA; 758 MW; 69D2C1E952D1B2AC CRC64;

Query Match 28.1%; Score 9; DB 10; Length 7;
 Best Local Similarity 33.3%; Pred. No. 8.3e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 LTI 5
 DB 1 VTV 3

RESULT 6

Q8JE81 PRELIMINARY; PRT; 7 AA.
 AC Q8JE81;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Truncated pol protein (Fragment).
 GN POL.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviridae; Retrovirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=4874;
 RX MEDLINE=22056123; PubMed=12560770;
 RA Beerwinkler N., Schmidt B., Walter H., Kaiser R., Longauer T.,
 RA Hoffmann C., Korr K., Selbig C.;
 RA "Diversity and complexity of HIV-1 drug resistance: A bioinformatics
 approach to predicting phenotype from genotype";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
 DR EXBL: AF347267; AA33344.1; -;
 FT NON TER 1
 SQ SEQUENCE 7 AA; 555 MW; 76C37731A04C700 CRC64;

Query Match 29.1%; Score 9; DB 15; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TS 3
 DB 4 TL 5

RESULT 7
 P82181
 ID P82181 PRELIMINARY; PRT; 6 AA.
 AC P82181;

DT 01-JUN-2000 (TREMBLrel. 14, Created)
 DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
 OS Spinacia oleracea (Spinach).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]

RP SEQUENCE.
 RC STRAIN=cv. ALVARO; TISSUE=Leaf;
 RX MEDLINE=20435798; PubMed=10874046;
 RA Yamaguchi K., Subramanian A.R.;

RA "The plastid ribosomal proteins. Identification of all the proteins in
 the 50 S subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28466-28482(2000).
 DE 3'-methylcephem hydroxylase (Fragment).
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro; IPR001790; Ribosomal_L10.
 DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
 DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON TER 6
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 25.0%; Score 8; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IS 6
 DB 2 IS 3

RESULT 8
 P82182
 ID P82182 PRELIMINARY; PRT; 6 AA.
 AC P82182;

DT 01-JUN-2000 (TREMBLrel. 14, Created)
 DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
 OS Spinacia oleracea (Spinach).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. ALVARO; TISSUE=Leaf;
 RX MEDLINE=20435798; PubMed=10874046;
 RA Yamaguchi K., Subramanian A.R.;

RA "The plastid ribosomal proteins. Identification of all the proteins in
 the 50 S subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28466-28482(2000).
 DE 3'-methylcephem hydroxylase (Fragment).
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro; IPR001790; Ribosomal_L10.
 DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
 DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON TER 6
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 25.0%; Score 8; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IS 6
 DB 2 IS 3

RESULT 9
 P72081
 ID P72081 PRELIMINARY; PRT; 7 AA.
 AC P72081;

DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 3'-methylcephem hydroxylase (Fragment).
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro; IPR001790; Ribosomal_L10.
 DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
 DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON TER 6
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 25.0%; Score 8; DB 2; Length 7;
 Best Local Similarity 33.3%; Pred. No. 8.3e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISS 7
 DB 5 VTS 7

RESULT 10
 Q47029
 ID Q47029 PRELIMINARY; PRT; 7 AA.
 AC Q47029;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update);
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update);
 DE Aad Al protein (Fragment).
 GN Aad Al.
 OS Enterobacteriaceae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Enterobacter.
 OX NCBI_TaxID=550;
 RN [1].
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94079349; PubMed=8257126;
 RA Rather P.N., Vaut P.A., Mierzwa R., Haze R.S., Miller G.H., Shaw K.J.;
 RT "Analysis of the aac(3)-Via gene encoding a novel 3-N-
 RT acetyltransferase".
 RL Antimicrob. Agents Chemother. 37:2074-2079(1993).
 DR EMBL; M88012; AAA6193.1; -;
 FT NON TER 1 1
 SQ SEQUENCE 7 AA; 744 MW; 63386202C321A030 CRC64;

Query Match 21.9%; Score 7; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 IT 4
 DB 1 IT 2

RESULT 11
 Q65578 PRELIMINARY; PRT; 7 AA.
 AC Q65578;
 DT 01-NOV-1996 (TREMBLrel. 01, Created);
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update);
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update);
 DE Hypothetical 0.8 kDa protein (fragment).
 OS Bovine herpesvirus 1.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesvirinae;
 OC Alphaherpesvirinae; Varicellovirus.
 OX NCBI_TaxID=10120;
 RN [1].
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cooper;
 RX MEDLINE=95313343; PubMed=7793062;
 RA Vleck C., Bensch V., Lu Z., Kutish G.F., Patten V., Rock D.,
 RA Letchworth G.J., Schwyer M.;
 RT "Nucleotide sequence analysis of a 10-kb region of the bovine
 RT herpesvirus genome which exhibits a colinear gene arrangement with
 RT the UL21 to UL4 genes of herpes simplex virus.";
 RL Virology 210:100-108(1995).
 DR EMBL; Z48053; CAA68130.1; -;
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 7 AA; 758 MW; 6D533455B1F1P1CC CRC64;

Query Match 21.9%; Score 7; DB 12; Length 7;
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TISS 7
 DB 1 TTHS 4

RESULT 12
 P83308 PRELIMINARY; PRT; 5 AA.
 AC P83308;
 DT 01-JUN-2002 (TREMBLrel. 21, Created);
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update);
 DE FMRFamide-like neuropeptide (LPLAF-amide).
 OS Gallus gallus (Chicken).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OX NCB: TaxID=9031;
 RN [1].
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RX PubMed=6137771;
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
 RT "A novel active pentapeptide from chicken brain identified by
 RT antibodies to FMRFamide".
 RJ Nature 305:328-330(1983).
 CC 1- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
 CC 1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA; 645 MW; 69D407376740C000 CRC64;

Query Match 18.8%; Score 6; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 DB 5 F 5

RESULT 13
 P82541 PRELIMINARY; PRT; 6 AA.
 AC P82541;
 DT 01-OCT-2000 (TREMBLrel. 15, Created);
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update);
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update);
 DE Chloroplast 30S ribosomal protein S19 beta (fragment).
 CS Spinacia oleracea (Spinach);
 CG Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons;
 CC Caryophyllales; Caryophyllaceae; Chenopodiaceae; Spinacia.
 OX NCB: TaxID=3562;
 RN [1].
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC STRAIN=CV. ALVARO; TISSUE=Leaf;
 RX MEDLINE=20435797; PubMed=10874039;
 RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
 RT "The plastid ribosomal proteins: Identification of all the proteins in
 RT the small subunit of an organelle ribosome (chloroplast)",
 RL J. Biol. Chem. 273:28455-28465(2000).
 CC 1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
 CC 1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC 1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC 1- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
 CC 1- MASS SPECTROMETRY: MW=10495; METHOD=VALDI.
 CC 1- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
 CC FORM IS THE MINOR BASIC FORM.
 CC 1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
 CC 1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR002222; Ribosomal S-9.
 DR Pfam: PF00203; Ribosomal S19; PARTIAL.
 DR PRINTS: PR00375; RIBOSOMALS19; PARTIAL.
 DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON TER 6
 SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 18.8%; Score 6; DB 10; Length 6;
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TIS 6
 DB 1 TRS 3

Search completed: October 4, 2003, 12:48:31
Job time : 50 secs

RESULT 14

OS0556 PRELIMINARY: PRT: 7 AA.
ID OS0556
AC OS0556;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Giya (Fragment).
GN GYA.
OS Actinobacillus actinomycetemcomitans (Haemophilus actinomycetemcomitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33384;
RX MEDLINE=96355846; PubMed=8751884;
RA Kolodrubetz E., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C., Kraig E.;
RT "cis Elements and trans factors are both important in strain-specific regulation of the leukotoxin gene in Actinobacillus actinomycetemcomitans.";
RT Infect. Immun. 64:3451-3460(1996).
RL EMBL: U51862; AAB88721.1; -;
RN NON TER 1;
FT
SQ SEQUENCE 7 AA; 832 MW; 6DCB42D76734C420 CRC64;

Query Match 18.8%; Score 6; DB 2; Length 7;

Best Local Similarity 31.3%; Pred. No. 8.3e+05;

Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LT: 5

Db 3 LPV 5

RESULT 15

Q8KMS9 PRELIMINARY: PRT: 7 AA.
ID Q8KMS9
AC Q8KMS9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative transposase (Fragment).
GN TNA.
OS Enterobacter sp. CH2-4.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
CX NCBI_TaxID=143777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CH2-4;
RX MEDLINE=21604134; PubMed=11763242;
RA Mindlin S.Z., Kolodil G.Y., Gorlenko Z.M., Minakhina S.V., Minakhin L.S., Kalyaeva E.S., Kopteva A.V., Petrova V.A., Yurieva O.V., Nikiforov V.G.;
RT "Mercury resistance transposons of Gram-negative environmental bacteria and their classification".
RT Res. Microbiol. 152:811-822(2001).
RL EMBL: AJ302778; CAC83658.1; -;
RN NON TER 1;
FT
SQ SEQUENCE 7 AA; 966 MW; 737B1B1046DAA9A0 CRC64;

Query Match 18.8%; Score 6; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F:

Db 1 F:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:28:27 : Search time 51.6667 seconds
(without alignments)
21.595 Million cell updates/sec

Title: US-09-712-819c-1

Perfect score: 32

Sequence: 1 FTLTSS ?

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107563 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 75613

Minimum DB seq length: 6

Maximum DB seq length: ?

Post-processing: Minimum Match 3%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq 10Jun03.*

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23:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	28	87.5	7	20	AA45736
2	28	87.5	7	21	AA830076
3	25	78.1	7	20	AA45737
4	25	78.1	7	21	AA830075
5	24	75.0	7	20	AA45736
6	24	75.0	7	21	AA830074
7	21	65.6	7	20	AA45735
8	21	65.6	7	21	AA830073
9	20	62.5	5	23	AA85454

10	59.4	6	22	AA551422	Integrin activation
11	56.2	7	19	AA559711	Typic 40 kD subu
12	56.2	7	21	AA564225	Cadherin-related n
13	56.2	7	23	ABB84102	Human single chain
14	53.1	5	24	ABJ12234	Streptococcal prot
15	53.1	5	24	ABJ12235	Streptococcal prot
16	53.1	6	18	AAW39453	Human T cell epit
17	53.1	6	19	AAW73158	Hexapeptide #13 bi
18	53.1	6	19	AAW73290	Hexapeptide #13 bi
19	53.1	6	24	AAE31832	Androgen receptor
20	53.1	7	11	AAAR7656	Ribonuclease reduc
21	53.1	7	23	AAAY40723	S1 derivative #20
22	53.1	7	21	AAAB30062	Scaffold protein S
23	53.1	7	22	AAW44200	H11 binding site c
24	53.1	7	22	AAW44205	H11 binding site c
25	50.0	6	10	AAAP93345	Portion of myc var
26	50.0	6	17	AAAR93089	GAL4 DNA binding d
27	50.0	6	19	AAW76753	Marine signalling
28	50.0	6	19	AAW61443	Gal 4 protein, 3'
29	50.0	6	20	AAW92487	Murine Gal4 prote
30	50.0	6	21	AAW01571	Nuclear chimeric co
31	50.0	6	21	AAW94491	Gal4 RNA binding d
32	50.0	6	22	AAAB68336	Peptide #16 encode
33	50.0	6	22	AAAB36561	Peptide #2 encode
34	50.0	6	23	AAE28111	Human immunoglobul
35	50.0	6	23	ABJ11455	Human 125P5C8 epit
36	50.0	6	24	ABR44966	Staphylococcus aur
37	50.0	6	24	ABR45358	Staphylococcus aur
38	50.0	6	24	ABR45694	Staphylococcus aur
39	50.0	6	24	ABR46086	Staphylococcus aur
40	50.0	6	24	ABR46479	Staphylococcus aur
41	50.0	6	24	ABR46870	Staphylococcus aur
42	50.0	7	16	AAW72775	Mammalian ribonuc
43	50.0	7	20	ABW76323	Cyclodextrin gluc
44	50.0	7	20	AAAY42013	Rheumatoid arthrit
45	50.0	7	20	AAAY45625	S1 derivative #6,

ALIGNMENTS

RESULT 1
AA45736
ID AA45738 standard; peptide; 7 AA.
XX
AC AA45735;
XX
DT 01-DEC-1999 (first entry)
XX
DE S4 derivative #12, beta strand of scaffold protein structure.
XX
KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
XX
KW tumour; chemotherapeutic agent.
XX
CS Synthetic.
XX
PN EP947582-A1.
XX
PC 06-OCT-1993.
XX
PF 31-MAR-1998; 98EP-0870365.
XX
PR 31-MAR-1998; 98EP-0870365.
XX
PA (INNO-) INNOGENETICS NV.
XX
FI Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX
DR WPI; 1999-542958/46.
XX
PT New scaffold protein, useful for stabilizing antigens used as vaccines
XX

CC target the complex to tumour cells. Another surface may be bound to a
CC cytotoxic molecule or an autoimmune antibody which may then kill the
CC tumour cells. Therefore the scaffold protein may be used to target
CC chemotherapeutic agents to specific cells. It may also be used to
CC stabilize individual peptides in a peptide library and may be used in
CC diagnostic techniques, and to stabilize antigens used as vaccines.

XX Sequence 7 AA;

Query Match 78.1%; Score 25; DB 20; Length 7;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy : FTLTIS 6
Db : FTLTIS 7

RESULT 4
AAB30075
D AAB30075 standard; Peptide; 7 AA.

X C AAB30075;

X T 09-FEB-2001 (first entry)

X Scaffold protein SCA S4 peptide SEQ ID NO: 136.

Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;
diabetic retinopathy; atherosclerosis.

XX Synthetic.

XX WO200060070-A1.

XX 12-OCT-2000.

XX 01-APR-1999; 99WO-EP02283.

XX 01-APR-1999; 99WO-EP02283.

XX (INNO-) INNOGENETICS NV.

Desmet J, Hufton S, Hoogenboom H, Sablon E;

WPI; 2000-66502/64.

Scaffold composed of single-chain polypeptide having beta sandwich
architecture carrying new and randomized peptide sequences useful as
supporting framework and carrying antigen- or receptor binding
fragments.

Disclosure; Page 15; 68pp; English.

The present invention is concerned with producing scaffold proteins
based upon the human CTLA-4 SCA domain. These scaffold proteins can be
used as a scaffold to bind antigen- or receptor-binding fragments. These
can be used in the treatment of diseases such as cancer,
atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and
diabetic retinopathy. Sequences AAB29930-B29939 were used in the
production of the proteins of the invention.

XX Sequence 7 AA;

Query Match 78.1%; Score 25; DB 21; Length 7;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy : FTLTIS 6
Db : FTLTIS 7

RESULT 6
AAB30074

RESULT 5
AAY40736
D AAY40736 standard; peptide; 7 AA.

XX AAY40736;

DT 01-DEC-1999 (first entry)

DE S4 derivative #10, beta strand of scaffold protein structure.

XX Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
tumour; chemotherapeutic agent.

XX Synthetic.

XX EP947582-A1.

XX 06-OCT-1999.

XX 31-MAR-1998; 98EP-0870065.

XX 31-MAR-1998; 98EP-0870065.

XX (INNO-) INNOGENETICS NV.

Desmet J, Hufton S, Hoogenboom H, Sablon E;

WPI; 1999-542958/46.

New scaffold protein, useful for stabilizing antigens used as vaccines

XX Disclosure; Page 6; 105pp; English.

Sequences AAY40727-Y40748 are functionally equivalent derivatives of the
S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a
beta strand peptide which forms part of a beta sheet. Peptides
(AAY40601-Y40609) together form a single-chain scaffold protein which
contains at least 1 disulfide bond, contains less than 10% alpha helix
and contains at least 6 beta-strands. The scaffold protein is constructed
of beta strands S1-S6, and may also include beta strands A1-A3, or any
functionally equivalent derivative of these sequences. The beta strands
form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to
the next by hydrogen bonds, which generate a beta sandwich architecture.
If the additional beta strands A1-A3 are included in the structure the
scaffold is constructed of two beta sheets, with the structures
A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each
other via amino acid loops, where at least one of the loops binds to a
receptor or antigen. The scaffold protein is used to stabilize antigens
or whole proteins such as receptors, or their fragments. It may be used
to bind two separate molecules. For example, one surface of the scaffold
may be bound to a protein which binds to a tumour antigen. This will
target the complex to tumour cells. Another surface may be bound to a
cytotoxic molecule or an autoimmune antibody which may then kill the
tumour cells. Therefore the scaffold protein may be used to target
chemotherapeutic agents to specific cells. It may also be used to
stabilize individual peptides in a peptide library and may be used in
diagnostic techniques, and to stabilize antigens used as vaccines.

XX Sequence 7 AA;

Query Match 75.0%; Score 24; DB 20; Length 7;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy : FTLTIS 6
Db : FTLTIS 7

ID AAB30074 standard; Peptide; 7 AA.
 XX
 AC AAB30074;
 XX
 DT 09-FEB-2001 (first entry)
 XX
 DE Scaffold protein SCA S4 peptide SEQ ID NO: 135.
 XX
 DE Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
 KW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;
 KW diabetic retinopathy; atherosclerosis.
 XX
 OS Synthetic.
 XX
 PN WO200060070-A1.
 XX
 PD 12-OCT-2000.
 XX
 PF 01-APR-1999; 99WO-EF02283.
 XX
 PR 01-APR-1999; 99WO-EP02283.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
 XX
 DR WPI; 2000-665002/64.
 XX
 PT Scaffold composed of single-chain polypeptide having beta sandwich
 PT architecture carrying new and randomized peptide sequences useful as
 PT supporting framework and carrying antigen- or receptor binding
 PT fragments -
 XX
 PS Disclosure; Page 15; 68pp; English.
 XX
 XX The present invention is concerned with producing scaffold proteins
 CC based upon the human CTLA-4 SCA domain. These scaffold proteins can be
 CC used as a scaffold to bind antigen- or receptor-binding fragments. These
 CC can be used in the treatment of diseases such as cancer,
 CC atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and
 CC diabetic retinopathy. Sequences AAB29930-829939 were used in the
 CC production of the proteins of the invention.
 XX
 SQ Sequence 7 AA;
 XX
 Query Match 75.0%; Score 24; DB 25; Length 7;
 Best Local Similarity 83.3%; Pred. No. 9.3e+55;
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 1 FTLLIS 6
 Db 2 FTLLIS 7
 RESULT 7
 AAY40735
 ID AAY40735 standard; peptide; 7 AA.
 XX
 AC AAY40735;
 XX
 DT 01-DEC-1999 (first entry)
 XX
 DE S4 derivative #9, beta strand of scaffold protein structure.
 DE
 KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
 KW tumour; chemotherapeutic agent.
 XX
 OS Synthetic.
 XX
 PN EP947582-A1.
 XX
 PD 06-OCT-1999.
 XX
 PF
 XX

PF 31-MAR-1998; 98EP-C870665.
 XX
 PR 31-MAR-1998; 98EP-C870665.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
 XX
 DR WPI; 1999-542958/46.
 XX
 PT New scaffold protein, useful for stabilizing antigens used as vaccines
 PT
 XX
 PS Disclosure; Page 6; 105pp; English.
 XX
 CC Sequences AAY40727-Y40748 are functionally equivalent derivatives of the
 CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a
 CC beta strand peptide which forms part of a beta sheet. Peptides
 CC (AAY45601-Y40609) together form a single-chain scaffold protein which
 CC contains at least 1 disulfide bond, contains less than 10% alpha helix
 CC and contains at least 6 beta-strands. The scaffold protein is constructed
 CC of beta strands S1-S6, and may also include beta strands A1-A3, or any
 CC functionally equivalent derivative of these sequences. The beta strands
 CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to
 CC the next by hydrogen bonds, which generate a beta sandwich architecture.
 CC If the additional beta strands A1-A3 are included in the structure the
 CC scaffold is constructed of two beta sheets, with the structures
 CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each
 CC receptor via amino acid loops, where at least one of the loops binds to a
 CC receptor or antigen. The scaffold protein is used to stabilize antigens
 CC or whole proteins such as receptors, or their fragments. It may be used
 CC to bind two separate molecules. For example, one surface of the scaffold
 CC may be bound to a protein which binds to a tumour antigen. This will
 CC target the complex to tumour cells. Another surface may be bound to a
 CC cytotoxic molecule or an autoimmune antibody which may then kill the
 CC tumour cells. Therefore the scaffold protein may be used to target
 CC chemotherapeutic agents to specific cells. It may also be used to
 CC stabilize individual peptides in a peptide library and may be used in
 CC diagnostic techniques, and to stabilize antigens used as vaccines.
 XX
 SQ Sequence 7 AA;
 XX
 Query Match 65.6%; Score 21; DB 25; Length 7;
 Best Local Similarity 66.7%; Pred. No. 9.3e+55;
 Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 FTLLIS 6
 Db 2 YSLTIS 7
 RESULT 8
 AAB30073
 ID AAB30073 standard; Peptide; 7 AA.
 XX
 AC AAB30073;
 XX
 DT 09-FEB-2001 (first entry)
 XX
 DE Scaffold protein SCA S4 peptide SEQ ID NO: 134.
 DE
 KW Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
 KW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;
 KW diabetic retinopathy; atherosclerosis.
 XX
 OS Synthetic.
 XX
 PN WO200060070-A1.
 XX
 PD 12-OCT-2000.
 XX
 PF 01-APR-1999; 99WO-EP02283.
 XX

PR 01-APR-1999; 99WO-BF02283.

XX (INNO-) INNOGENETICS NV.

XX Desmet J, Hufon S, Hoogenboom H, Sablon B;

XX WPI; 2000-665002/64.

XX Scaffold composed of single-chain polypeptide having beta sandwich
PT architecture carrying new and randomized peptide sequences useful as
PT supporting framework and carrying antigen- or receptor binding
PT fragments -

XX Disclosure; Page 15; 48pp; English.

XX The present invention is concerned with producing scaffold proteins
CC based upon the human CTA-4 SCA domain. These scaffold proteins can be
CC used as a scaffold to bind antigen- or receptor-binding fragments. These
CC can be used in the treatment of diseases such as cancer,
CC atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and
CC diabetic retinopathy. Sequences AAB2930-B2939 were used in the
CC production of the proteins of the invention.

XX SQ Sequence 7 AA;

Query Match 65.6%; Score 21; DB 21; Length 7;

Best Local Similarity 66.7%; Pred. No. 9.3e+05;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 2;

Qy 1 FTLTIS 6

Db :|||

2 YSLTIS 7

RESULT 9

AAU85454
ID AAU85454 standard; Peptide; 5 AA.

XX AAU85454;

XX 21-MAY-2002 (first entry)

XX Human colon specific polypeptide antibody binding site #31.
DE Human; colon specific gene; CSG; cytostatic; metastasis;
XX Human; colon cancer staging; antibody binding site.

XX Homo sapiens.

XX WO200206555-A2.

XX 24-JAN-2002.

XX 17-JUL-2001; 2001WO-US22454.

XX 17-JUL-2002; 2000US-0615596.

XX (DIAD-) DIADEXUS INC.

XX Macina RA, Sun Y;

XX WPI; 2002-171815/22.

XX Diagnosing, staging or monitoring colon cancer involves determining a
PT colon specific gene in cells, tissues or body fluids in patient; and
PT comparing it with levels of the gene from a normal human control -
XX Disclosure; Page 21; 52pp; English.

XX The invention relates to diagnosing the presence of colon cancer,
CC metastases of colon cancer, staging colon cancer, monitoring colon cancer
CC for the onset of metastasis or monitoring a change in stage of colon
CC cancer in a patient. The method involves determining a colon specific

CC gene (CSG) in cells, tissues or bodily fluids and comparing it with
CC levels of CSG in cells, tissues or bodily fluids from a normal human
CC control. Colon cancer can be treated by administering a molecule which
CC down regulates the expression or activity of CSG. An immune response
CC against a target cell expressing CSG can be induced by delivering an
CC immunologically stimulatory amount of a CSG protein to a patient, so that
CC an immune response is mounted. Therapeutic agents are useful for imaging
CC colon cancer in a patient by administering an agent labelled with
CC paramagnetic ions or a radioisotope to the patient. They are also useful
CC for preventing the onset of colon cancer and in diagnosis and treatment
CC of the disease. Sequences AAU85424-AAU85502 represent human colon
CC specific protein antibody binding sites used in the method of the
CC invention.

XX SQ Sequence 5 AA;

Query Match 62.5%; Score 20; DB 23; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLT 4

Db :|||

2 FTLT 5

RESULT 10

AAU851422
ID AAU851422 standard; peptide; 6 AA.

XX AAU851422;

XX 08-JAN-2002 (first entry)

XX Integrin activating peptide SEQ ID NO 1.

XX Integrin stimulant; vulnary; injury healing;

XX postsurgical tissue recovery.

XX Unidentified.

XX JP2001213898-A.

XX 07-AUG-2001.

XX 31-JAN-2000; 2000JP-0022469.

XX 31-JAN-2000; 2000JP-0022469.

XX (HISM) HISAMITSU PHARM CO LTD.

XX WPI; 2001-629610/73.

XX An injury healing and postsurgical tissue recovering integrin

XX activating peptide -

XX Claim 1; Page 3; 11pp; Japanese.

XX The invention relates to novel peptides with vulnary activity, useful
CC for injury healing and postsurgical tissue recovery by acting as an
CC integrin stimulant.

XX SQ Sequence 6 AA;

Query Match 59.4%; Score 19; DB 22; Length 6;

Best Local Similarity 60.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTI 5

Db :|||

YTLTI 5

RESULT 11

|||||
1 FTIDSSS 7

RESULT 13

AB884102

D AB884102 standard; Protein: 7 AA.

XX AB884102;

XX 09-SEP-2002 (first entry)

XX Human single chain diabody C8Aa1 fragment #2.

XX Antibody; multimer; Cytostatic; detection; immunoassay; tumour.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 6 /note= "Unidentified residue"

XX DE10060140-A1.

XX 06-JUN-2002.

XX 04-DEC-2000; 2000DE-1050140.

XX 04-DEC-2000; 2000DE-1050140.

XX (VECT-) VECTRON THERAPEUTICS INT AG.

XX Kontermann R;

XX WPI; 2002-520384/56.

XX New multimer of single-chain antibodies, useful e.g. for diagnosis or

XX drug delivery, has four variable chains linked through peptides of

XX controlled length .

XX Example 1; Fig 2B; 16pp; German.

XX This invention describes a novel multimer containing at least two

XX antibodies, each, independently, comprising a polypeptide chain of

XX structure V1-PA-V2-PM-V3-PB-V4 where V1-V4 = variable domains; PA, PB

XX and PM = peptide linkers with PA and PB containing 0 or 1 amino acid. The

XX products of the invention have cytostatic activity. The multimers

XX described can be used for diagnostic detection, in essentially standard

XX immunoassay methods, and for binding at least one component and/or fused

XX protein or peptide to a cell, especially to deliver a toxin or for

XX infection, transformation or transfection of the cell. (i), or nucleic

XX acid (ii) encoding it, or vectors containing (ii), are useful for

XX treating tumours. The multimers are relatively small (about 1.0 kDa for a

XX dimer) but have multiple binding sites to ensure high binding affinity.

XX This sequence represents a fragment of the single chain diabody C8Aa-

XX (composed of a tumour marker carcinoembryonic antigen fragment and

XX E. coli beta-galactosidase fragment) described in the method of the

XX invention.

XX Sequence 7 AA;

XX Query Match

XX Best Local Similarity 56.2%; Score 19; DB 23; Length 7;

XX Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

XX 2 TLTIIS 6

XX 1 TVIVS 5

XX RESULT 14

XX ABU12234

D ABU12234 standard; Peptide; 5 AA.

XX

AC ABU12234;

XX

CT 18-FEB-2003 (first entry)

XX

DE Streptococcal protein G, IGB1, alpha helix prediction pentapeptide #51.

XX

KW ASTRO-FOLD; ab initio; alpha-helix; beta-sheet; disulphide bridge;

KW atomistic modelling; low energy conformation; entropic energy;

KW free energy; equilibrium probability; helical cluster; integer-linear;

KW mathematical model; hydrophobic contact energy;

KW atom force field potential; Global optimisation; torsion angle;

KW dynamic algorithm; three-dimensional structure; tertiary structure;

KW immunoglobulin-binding domain; protein G; IGB1.

XX

CS Streptomyces griseus.

XX

FN W0200279872-A2.

XX

PD 10-OCT-2002.

XX

PF 19-FEB-2002; 2002WO-US04644.

XX

PR 16-FEB-2001; 2001US-0798006.

XX

PA (UYPB-) UNIV PRINCETON.

XX

PI Floudas CA, Klepeis JL;

XX

DR WPI; 2003-058449/05.

XX

PT Determining helix regions, and beta sheets of polypeptide, involves

PT partitioning peptide, atomistic modeling by selected force, generating

PT ensemble low energy, and calculating free energies for each peptide

XX

PS Example 1; Page 59; 147pp; English.

XX

CC The invention discloses a ASTRO-FOLD approach for the ab initio

CC prediction method for determining the existence and location of

CC alpha-helix regions and arrangement of beta-sheets and disulphide bridges

CC of a polypeptide. The method comprises defining the first segment of the

CC amino acid sequence, performing atomistic modelling upon each segment,

CC generating an ensemble of low energy conformations, determining the

CC entropic and free energy for each segment and then ascertaining the

CC equilibrium probabilities for helical clusters. The segments consist of

CC pentapeptides, with each further segment including a majority of the

CC amino acid residues of the first segment, together with an additional

CC amino acid residue(s), adjacent to the first amino acid sequence. The

CC beta-sheets and disulphide bridges of a polypeptide are determined by

CC identifying a superstructure encompassing alternative beta-strand

CC arrangements, representing the superstructure by an integer-linear

CC programming mathematical model, with the model maximising the total

CC also apply energy modelling, with a full atom force field potential to

CC generate a constrained global optimisation problem, optionally applying a

CC torsion angle dynamics algorithm and then solving the constrained global

CC optimisation problem to determine the three-dimensional structure of the

CC polypeptide. The method is useful for determining the tertiary structure

CC of a polypeptide and is accurate and reliable. The sequences presented in

CC ABU12184-ABU12235 are the pentapeptides of the Streptomyces griseus

CC immunoglobulin-binding domain from streptococcal protein G, IGB1, which

CC were used to predict the alpha-helical regions in an example of the

XX method of the invention.

XX Sequence 5 AA;

XX Query Match

XX Best Local Similarity 53.1%; Score 17; DB 24; Length 5;

XX Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX 1 FTLT 4

XX 2 FTVT 5

XX

XX

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy - FTVT 4
Db 1 FTVT 4Search completed: October 4, 2003, 12:45:22
Job time : 53.6667 secs

RESULT 15
ABU12235
ID ABU12235 standard; Peptide; 5 AA.
AC ABU12235;
XX
DT 19-FEB-2003 (first entry)
XX
DE Streptococcal protein G, IGB1, alpha helix prediction: pentapeptide #52.
XX
KW ASTRO-FOLD; ab initio; alpha-helix; beta-sheet; disulphide bridge;
KW atomistic modeling; low energy conformation; entropic energy;
KW free energy; equilibrium probability; helical cluster; integer-linear;
KW mathematical model; hydrophobic contact energy;
KW atom force field potential; global optimisation; torsion angle;
KW dynamic algorithm; three-dimensional structure; tertiary structure;
KW immunoglobulin-binding domain; protein G; IGB1.
XX
OS Streptomyces griseus.
XX
PN WO200279872-A2.
XX
PD 10-OCT-2002.
XX
PF 19-FEB-2002; 2002WO-US04644.
XX
PR 16-FEB-2001; 2001US-0788006.
XX
PA (CYPR-) UNIV PRINCETON.
XX
PI Floudas CA, Kiepeis JI;
XX
DR WPI; 2003-058449/05.
XX
PT Determining helix regions, and beta sheets of polypeptide, involves
PT partitioning peptide, atomistic modeling by selected force, generating
PT ensemble low energy, and calculating free energies for each peptide -
XX
PS Example 1; Page 59; 147pp; English.

The invention discloses a ASTRO-FOLD approach for the ab initio
prediction method for determining the existence and location of
alpha-helix regions and arrangement of beta-sheets and disulphide bridges
of a polypeptide. The method comprises defining the first segment of the
amino acid sequence, performing atomistic modeling upon each segment,
generating an ensemble of low energy conformations, determining the
entropic and free energy for each segment and then ascertaining the
equilibrium probabilities for helical clusters. The segments consist of
pentapeptides, with each further segment including a majority of the
amino acid residues of the first segment, together with an additional
amino acid residue; adjacent to the first amino acid sequence. The
beta-sheets and disulphide bridges of a polypeptide are determined by
identifying a superstructure encompassing alternative beta-strand
arrangements, representing the superstructure by an integer-linear
programming mathematical model, with the model maximising the total
hydrophobic contact energy, and then solving the model. The method can
also apply energy modelling with a full atom force field potential to
generate a constrained global optimisation problem, optionally applying a
torsion angle dynamics algorithm and then solving the constrained global
optimisation problem to determine the three-dimensional structure of the
polypeptide. The method is useful for determining the tertiary structure
of a polypeptide and is accurate and reliable. The sequences presented in
ABU12184-ABU12235 are the pentapeptides of the Streptomyces griseus
immunoglobulin-binding domain from streptococcal protein G, IGB1, which
were used to predict the alpha-helical regions in an example of the
method of the invention.

SQ Sequence 5 AA;

Query Match 53.1%; Score 17; DB 24; Length 5;
Best Local Similarity 75.0%; Pred. No. 9.3e+05;

GenCore version 5.1.6
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OM protein - protein search, using sw mode:

Run on: October 4, 2003, 12:48:43 ; Search time 33.6667 Seconds
(without alignments)
32.896 Million cell updates/sec

Title: US-09-712-819c-1

Perfect score: 32

Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62

Gapof 10.0 , Gapext 0.5

Searched: 587654 seqs, 15822981 residues

Total number of hits satisfying chosen parameters: 33362

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/FCI_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US0A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US0B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	length	ID	Description
1	18	56.2	7	15	US-10-006-869-637
2	17	53.1	5	11	US-09-788-006-107
3	17	53.1	5	11	US-09-788-006-107
4	17	53.1	5	15	US-10-154-971-29
5	17	53.1	6	10	US-09-777-921A-17
6	17	53.1	6	11	US-09-530-139-14
7	17	53.1	6	14	US-10-156-820-59
8	17	53.1	6	15	US-10-097-175-97
9	16	50.0	4	12	US-10-159-906-47
10	16	50.0	7	9	US-09-832-723-69
11	16	50.0	7	10	US-09-996-288-164
12	16	50.0	7	11	US-09-996-265-164
13	16	50.0	7	12	US-10-303-331-69
14	16	50.0	7	12	US-10-022-056-214
15	15	46.9	5	12	US-10-286-186-3

16	15	46.9	5	12	US-10-286-186-4	Sequence 4, Appl
17	15	46.9	5	12	US-10-315-84A-394	Sequence 394, App
18	15	46.9	5	12	US-10-317-252A-394	Sequence 394, App
19	15	46.9	5	12	US-10-317-252A-394	Sequence 394, App
20	15	46.9	6	9	US-09-876-388-6	Sequence 6, Appl
21	15	46.9	6	12	US-10-315-964A-402	Sequence 402, App
22	15	46.9	6	12	US-10-317-251A-402	Sequence 402, App
23	15	46.9	6	12	US-10-317-252A-402	Sequence 402, App
24	15	46.9	6	15	US-10-185-932-39	Sequence 39, Appl
25	15	46.9	6	15	US-10-306-869-850	Sequence 650, App
26	15	46.9	6	15	US-10-287-852-6	Sequence 6, Appl
27	15	46.9	6	15	US-10-288-343-6	Sequence 6, Appl
28	15	46.9	7	9	US-09-056-162B-5	Sequence 5, Appl
29	15	46.9	7	9	US-09-056-162B-124	Sequence 124, App
30	15	46.9	7	9	US-09-876-388-7	Sequence 7, Appl
31	15	46.9	7	9	US-09-734-417-12	Sequence 12, Appl
32	15	46.9	7	10	US-09-095-881-9	Sequence 8, Appl
33	15	46.9	7	10	US-09-947-137-7	Sequence 7, Appl
34	15	46.9	7	10	US-09-996-288-133	Sequence 133, App
35	15	46.9	7	10	US-09-996-288-135	Sequence 135, App
36	15	46.9	7	10	US-09-996-288-160	Sequence 160, App
37	15	46.9	7	11	US-09-223-751A-53	Sequence 53, Appl
38	15	46.9	7	11	US-09-223-751A-54	Sequence 54, Appl
39	15	46.9	7	11	US-09-996-285-133	Sequence 133, App
40	15	46.9	7	11	US-09-996-265-160	Sequence 160, App
41	15	46.9	7	11	US-10-169-351-8	Sequence 8, Appl
42	15	46.9	7	12	US-10-286-457-210	Sequence 210, App
43	15	46.9	7	14	US-10-050-552A-4	Sequence 4, Appl
44	15	46.9	7	14	US-10-006-869-637	Sequence 637, App
45	15	46.9	7	15	US-10-006-869-637	Sequence 637, App

ALIGNMENTS

RESULT 1
US-10-006-869-637
; Sequence 637, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 637
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence

US-10-006-869-637
Query Match 56.2% Score 18; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 5.3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qv : FTLTSS 7
||: ||
Db : FTLTSS 7

RESULT 2
US-09-788-006-107
; Sequence 107, Application US/09788006
; Publication No. US20030036093A1

```

; GENERAL INFORMATION:
; APPLICANT: Floudas, Christopher A.
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
; FILE REFERENCE: PU-0607
; CURRENT APPLICATION NUMBER: US/09/788,006
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Streptomyces griseus
US-09-788-006-107

Query Match      53.1%   Score 17;   DB 11;   Length 5;
Best Local Similarity 75.0%;   Pred. No. 5.3e+05;
Matches 3;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

Qy      1 FTLT 4
Db      2 FTVT 5

RESULT 3
US-09-788-006-108
; Sequence 108, Application US/09788006
; Publication No. US2003003639A1
; GENERAL INFORMATION:
; APPLICANT: Floudas, Christopher A.
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
; FILE REFERENCE: PU-0607
; CURRENT APPLICATION NUMBER: US/09/788,006
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 108
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Streptomyces griseus
US-09-788-006-108

Query Match      53.1%   Score 17;   DB 11;   Length 5;
Best Local Similarity 75.0%;   Pred. No. 5.3e+05;
Matches 3;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

Qy      1 FTLT 4
Db      2 FTVT 5

Query Match      53.1%   Score 17;   DB 15;   Length 5;
Best Local Similarity 60.6%;   Pred. No. 5.3e-05;
Matches 3;   Conservative 2;   Mismatches 0;   Indels 0;   Gaps 0;

Qy      3 LTSS 7
Db      1 VTSS 5

RESULT 5
US-09-777-921A-17
; Sequence 17, Application US/09777921A
; Patent No. US2002011536A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-777-921A-17

Query Match      53.1%   Score 17;   DB 10;   Length 6;
Best Local Similarity 100.0%;   Pred. No. 5.3e-05;
Matches 4;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy      3 LTSS 6
Db      2 LTSS 5

RESULT 6
US-09-530-139-14
; Sequence 14, Application US/09530139
; Publication No. US20030092892A1

```

GENERAL INFORMATION:
APPLICANT: FRENKEN, LEON GERARDUS
APPLICANT: HOWELL, STEVEN
APPLICANT: LEDERBOER, ADRIANUS MARINUS
APPLICANT: VAN DER LOOT, CORNELIS PAUL
TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS

FILE REFERENCE: 60113/268075/ASH
CURRENT APPLICATION NUMBER: US/09/530,139
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 1998-12-27
PRIOR APPLICATION NUMBER: PCT/EP98/04991
PRIOR FILING DATE: 1997-10-27
NUMBER OF SEQ ID NOS: 77

SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 14
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-530-139-14

Query Match 53.1%; Score 17; DB 14; Length 6;
Best Local Similarity 80.0%; Pred. No. 5.3e-05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTSS 7
DB 2 VTSS 6

RESULT 7

US-10-156-820-59
Sequence 59, Application US/10156820
Publication No. US2002050558A1

GENERAL INFORMATION:

APPLICANT: Boulanger, Pierre
APPLICANT: Hong, Saw See
APPLICANT: Karayan, Lucie
TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
FILE REFERENCE: 032751-036
CURRENT APPLICATION NUMBER: US/10/156,820

CURRENT FILING DATE: 2002-06-30
PRIOR APPLICATION NUMBER: PCT/FR95/00164
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: FR 97/01035
PRIOR FILING DATE: 1997-01-30
PRIOR APPLICATION NUMBER: FR 97/11166
PRIOR FILING DATE: 1997-09-09

NUMBER OF SEQ ID NOS: 98
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 59
LENGTH: 6

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Phagotome

US-10-156-820-59

Query Match 53.1%; Score 17; DB 14; Length 6;
Best Local Similarity 75.0%; Pred. No. 5.3e-05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLL 4
DB 3 YTLT 6

RESULT 8

US-10-097-175-97

Sequence 97, Application US/10097175

Publication No. US20030045680A1
GENERAL INFORMATION:
APPLICANT: JOYAL, JOHN L.
APPLICANT: MUELLER, JOHN
APPLICANT: OZA, VIBHA B.
APPLICANT: FINDEIS, MARK A.
TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR
FILE REFERENCE: PPI-110
CURRENT APPLICATION NUMBER: US/10/097,175
PRIOR FILING DATE: 2002-03-12
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/275,240
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/352,399
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 102

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 97

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Androgen Receptor Binding Polypeptides

US-10-097-175-97

Query Match 53.1%; Score 17; DB 15; Length 6;

Best Local Similarity 80.0%; Pred. No. 5.3e-05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LTSS 7
DB 1 LTSS 5

RESULT 9

US-10-159-006-47

Sequence 47, Application US/10159006

Publication No. US2003014329A1

GENERAL INFORMATION:

APPLICANT: Park, John B.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: Fc γ -specific Antibody with Improved Producibility

FILE REFERENCE: 0652.1890002

CURRENT APPLICATION NUMBER: US/10/159,006

CURRENT FILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: US 09/301,593

PRIOR FILING DATE: 1999-04-29

PRIOR APPLICATION NUMBER: EP 98107925.4

PRIOR FILING DATE: 1998-04-30

PRIOR APPLICATION NUMBER: US 60/086,049

PRIOR FILING DATE: 1998-05-18

NUMBER OF SEQ ID NOS: 108

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 47

LENGTH: 4

TYPE: PRT

ORGANISM: Homo sapiens

US-10-159-006-47

Query Match 50.0%; Score 16; DB 12; Length 4;

Best Local Similarity 75.0%; Pred. No. 5.3e-05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TSS 7
DB 1 TVSS 4

RESULT 10

US-09-832-723-69

Sequence 69, Application US/09832723
Patent No. US20020098524A1
GENERAL INFORMATION:
APPLICANT: Escott, David A.
APPLICANT: Chen, Yiyou
APPLICANT: Murray, Christopher J.
APPLICANT: Tjeterina, Pilar
TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
FILE REFERENCE: GC617-2
CURRENT APPLICATION NUMBER: US/09/532,723
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: US 63/197,259
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 117
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 69
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptides screened from a phage display random
peptide library

US-09-832-723-69

Query Match: 50.0%; Score 16; DB 9; Length 7;
Best Local Similarity 75.0%; Pred. No. 5.3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLTIS 7
DB 2 TLTIS 7

RESULT 11

US-09-996-288-164
Sequence 164, Application US/09096288
Patent No. US20020177126A1
GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.1
SEQ ID NO 164
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-09-996-288-164

Query Match: 50.0%; Score 16; DB 10; Length 7;
Best Local Similarity 50.0%; Pred. No. 5.3e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLTIS 7
DB 2 TMLSS 7

RESULT 12

US-09-996-265-164
Sequence 164, Application US/09096265
Patent No. US2003003584A1
GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,265
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.1
SEQ ID NO 164
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-09-996-265-164

FILE REFERENCE: 10271-048-999
CURRENT APPLICATION NUMBER: US/09/996,265
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.1
SEQ ID NO 164
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-09-996-265-164

Query Match: 50.0%; Score 16; DB 11; Length 7;
Best Local Similarity 50.0%; Pred. No. 5.3e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLTIS 7
DB 2 TMLSS 7

RESULT 13

US-10-303-331-69
Sequence 69, Application US/10303331
Publication No. US20030152976A1
GENERAL INFORMATION:
APPLICANT: Janssen, Giselle G.
APPLICANT: Murray, Christopher J.
APPLICANT: Winetzk, Deborah S.
TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
FILE REFERENCE: GC617-3
CURRENT APPLICATION NUMBER: US/10/303,331
CURRENT FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: US 09/832,723
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/197,259
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 69
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptides screened from a phage display random
peptide library
US-10-303-331-69

Query Match: 50.0%; Score 16; DB 12; Length 7;
Best Local Similarity 75.0%; Pred. No. 5.3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLTIS 7
DB 2 TLTIS 7

RESULT 14

US-10-022-066-214
Sequence 214, Application US/10322066
Publication No. US20030166057A1
GENERAL INFORMATION:
APPLICANT: HILDEBRAND, WILLIAM H.
APPLICANT: PRILLIMAN, KILEY RAE
TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 6680.034
CURRENT APPLICATION NUMBER: US/10/022,066
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/256,410
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/256,409
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 09/465,321

PRIOR FILING DATE: 1999-12-17
 PRIOR APPLICATION NUMBER: 09/974,365
 PRIOR FILING DATE: 2001-10-10
 NUMBER OF SEQ ID NOS: 638
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 214
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide
 US-10-022-086-214

Query Match 50.0% Score 16; DB 12; Length 7;
 Best Local Similarity 50.0%; Pred. No. 5.3e+05;
 Matches 3; Conservative 2; Mismatches 1; Indels 3; Gaps 0;

QY 2 FTLSS 7
 DB 1 TMTAAS 6

RESULT 15
 JS-10-286-186-3
 ; Sequence 3, Application US/0286186
 ; Publication No. US2003014374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PALMER, KENNETH E.
 ; APPLICANT: BOGUE, GARY P.
 ; TITLE OF INVENTION: ROLLING CIRCLE REPLICON EXPRESSION
 ; FILE REFERENCE: 008010179000US00
 ; CURRENT APPLICATION NUMBER: US/10/286,186
 ; PRIOR FILING DATE: 2002-11-01
 ; PRIOR APPLICATION NUMBER: US/09/505,477
 ; PRIOR FILING DATE: 2003-02-16
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Circovirus
 US-10-286-186-3

Query Match 46.9% Score 15; DB 12; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FTL 3
 DB 1 FTL 3

Search completed: October 4, 2003, 13:05:03
 Job time : 34.6867 secs

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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:42:47 : Search time 17 Seconds
(without alignments)
17,422 Million cell updates/sec

Title: US-09-712-819C-1

Perfect score: 32

Sequence: 1 FTUTISS 7

Scoring table: B:OSUM62

Gapop 13.0 , Gapext 0.5

Searched: 328717 seqs, 42310458 residues

Total number of hits satisfying chosen parameters: 4038

Minimum DB seq length: 3

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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4: /cgn2_6/prodata/1/aa/6B.COMB.pcp:*
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6: /cgn2_6/prodata/1/aa/backfiles.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	18	56.2	7	4	US-09-187-859-637
2	18	56.2	7	4	US-09-839-542B-637
3	17	53.1	5	3	US-08-757-177-16
4	17	53.1	6	4	US-09-155-613A-59
5	17	53.1	6	4	US-09-266-805-5
6	17	53.1	7	2	US-08-739-401A-6
7	16	50.0	4	3	US-08-860-904-9
8	16	50.0	4	4	US-09-301-593-47
9	16	50.0	6	1	US-08-252-995D-7
10	16	50.0	6	2	US-08-478-368A-46
11	16	50.0	6	2	US-08-252-597-46
12	16	50.0	6	2	US-08-388-653-46
13	16	50.0	6	2	US-08-473-985-46
14	16	50.0	6	2	US-08-834-108-7
15	16	50.0	6	2	US-08-483-898-46
16	16	50.0	6	3	US-09-087-716-46
17	16	50.0	6	3	US-09-157-753-46
18	16	50.0	6	3	US-09-157-230-46
19	16	50.0	6	3	US-09-087-811-46
20	16	50.0	6	3	US-09-156-855-46
21	16	50.0	6	3	US-09-158-010-46
22	16	50.0	6	3	US-09-087-647-46
23	16	50.0	6	4	US-09-302-629-46
24	16	50.0	7	1	US-08-136-741B-55
25	16	50.0	7	2	US-08-177-109A-7
26	16	50.0	7	2	US-08-667-706-7
27	16	50.0	7	3	US-09-040-216-28

Sequence 63, Appl
Sequence 22, Appl
Sequence 55, Appl
Sequence 17, Appl
Sequence 23, Appl
Sequence 26, Appl
Sequence 17, Appl
Sequence 23, Appl
Sequence 26, Appl
Sequence 62, Appl
Sequence 4, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 8, Appl
Sequence 54, Appl
Sequence 3, Appl
Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-187-859-637
; Sequence 637, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 637
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-187-859-637

Query Match 56.2%; Score 18; DB 4; Length 7;
Best Local Similarity 57.1%; Pred No. 2.5e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTUTISS 7
||: ||
DB 1 FTIDSS 7

RESULT 2

US-09-839-542B-637
; Sequence 637, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 637
; LENGTH: 7

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative linear modulating agent based on
OTHER INFORMATION: Catherin-related neuronal receptor cell adhesion
OTHER INFORMATION: recognition sequence
US-09-839-542B-637

Query Match 56.2%; Score 12; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 2.5e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLTS 7
Db 1 FTIDSS 7

RESULT 3
US-08-757-177-16
Sequence 16, Application US/08757177
Patent No. 6071718
GENERAL INFORMATION:
APPLICANT: MUKERJI, PRADIP
APPLICANT: HARDS, ROBERT G.
APPLICANT: THURMOND, JENNIFER M.
APPLICANT: LEONARD, AMANDA EUN-YEONG
TITLE OF INVENTION: METHODS OF PRODUCING A RECOMBINANT PROTEIN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,177
FILING DATE: 27-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,442
REFERENCE/DOCKET NUMBER: 6004.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-935-1723
TELEFAX: 847-938-2623

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-757-177-16

Query Match 53.1%; Score 17; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TISS 7
Db 2 TISS 5

RESULT 4
US-09-155-613A-59
Sequence 59, Application US/09155613A
Patent No. 6420120

GENERAL INFORMATION:
APPLICANT: Boulanger, Pierre
APPLICANT: Hong, Saw See
APPLICANT: Karayan, Lucie
TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
FILE REFERENCE: 032751-036
CURRENT APPLICATION NUMBER: US/09/155,613A
CURRENT FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: PCT/FR96/30284
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: FR 97/01005
PRIOR FILING DATE: 1997-01-30
PRIOR APPLICATION NUMBER: FR 97/11166
PRIOR FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 98
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 59
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Phagotome
US-09-155-613A-59

Query Match 53.1%; Score 17; DB 4; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLT 4
Db 3 YTLT 6

RESULT 5
US-09-266-805-5
Sequence 5, Application US/09266805
Patent No. 6517829
GENERAL INFORMATION:
APPLICANT: Unilever N.V.
APPLICANT: Unilever PLC
TITLE OF INVENTION: New products comprising inactivated yeasts or moulds
TITLE OF INVENTION: provided with active antibodies
FILE REFERENCE: t-7055
CURRENT APPLICATION NUMBER: US/09/266,805
CURRENT FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 5
LENGTH: 6
TYPE: PRT
ORGANISM: llama
US-09-266-805-5

Query Match 53.1%; Score 17; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTSS 7
Db 2 VTSS 6

RESULT 6
US-08-739-401A-6
Sequence 6, Application US/08739401A
Patent No. 5937461
GENERAL INFORMATION:
APPLICANT: Neitz, Maureen E.
APPLICANT: Neitz, John F.
TITLE OF INVENTION: DETECTION OF CONE-PHOTORECEPTOR-BASED
TITLE OF INVENTION: VISION DISORDERS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:

ADDRESSES: Quarles & Brady
 STREET: 411 East Wisconsin Avenue
 CITY: Milwaukee
 STATE: Wisconsin
 COUNTRY: U.S.A.
 ZIP: 53202-4497
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/739,4C1A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Baker, Sean C.
 REGISTRATION NUMBER: 35,433
 REFERENCE/DOCKET NUMBER: 650053.91151
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (414) 277-5709
 TELEFAX: (414) 277-3352
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-739-4C1A-6

Query Match 53.1%; Score 17; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLT 4
 |||
 DB 2 FTVT 5

RESULT 7
 US-08-860-904-9
 Sequence 9, Application US/08860904
 Patent No. 6294654
 GENERAL INFORMATION:
 APPLICANT: Sordlie, Irger
 APPLICANT: Bosen, Brianne
 APPLICANT: Fossum, Sigbjorn
 TITLE OF INVENTION: A Modified Immunoglobulin Molecule
 TITLE OF INVENTION: Incorporating an Antigen in a No. 6294654-CDR
 FILE REFERENCE: 9914-1
 CURRENT APPLICATION NUMBER: US/08/860,904
 CURRENT FILING DATE: 1997-09-29
 EARLIER APPLICATION NUMBER: PCT/GB96/00116
 EARLIER FILING DATE: 1996-01-19
 EARLIER APPLICATION NUMBER: GB 9501079.9
 EARLIER FILING DATE: 1995-01-19
 NUMBER OF SEQ ID NOS: 29
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 9
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Mus sp.
 US-08-860-904-9

Query Match 50.0%; Score 16; DB 3; Length 4;
 Best Local Similarity 75.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TISS 7
 |||
 DB 1 TVSS 4

RESULT 8
 US-09-301-593-47
 Sequence 47, Application US/09301593A
 Patent No. 6455677
 GENERAL INFORMATION:
 APPLICANT: Park, John E.
 APPLICANT: Garin-Chesa, Pilar
 APPLICANT: Bamberger, Uwe
 APPLICANT: Leger, Olivier
 APPLICANT: Saldanha, Jose W.
 APPLICANT: Rettig, Wolfgang C.
 TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
 FILE REFERENCE: 0652.1890001
 CURRENT APPLICATION NUMBER: US/09/301,593A
 CURRENT FILING DATE: 1999-04-29
 EARLIER APPLICATION NUMBER: EP 98107925.4
 EARLIER FILING DATE: 1998-04-30
 EARLIER APPLICATION NUMBER: US 60/086,049
 EARLIER FILING DATE: 1998-05-18
 NUMBER OF SEQ ID NOS: 108
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 47
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-301-593-47

Query Match 50.0%; Score 16; DB 4; Length 4;
 Best Local Similarity 75.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TISS 7
 |||
 DB 1 TVSS 4

RESULT 9
 US-08-252-995D-7
 Sequence 7, Application US/08252995D
 Patent No. 5650501
 GENERAL INFORMATION:
 APPLICANT: Dennis, James W
 APPLICANT: Heffernan, Mike
 APPLICANT: Fode, Carol
 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BERESKIN & PARR
 STREET: 40 King Street West
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/252,995D
 FILING DATE: 02-JUN-1994
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Kurdydko, Linda M
 REGISTRATION NUMBER: 34,971
 REFERENCE/DOCKET NUMBER: 3153-96
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 364-7311
 TELEFAX: (416) 361-1398
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:

```
/ LENGTH: 6 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Peptide
/ ORIGINAL SOURCE:
/ ORGANISM: Mus musculus
US-08-252-995D-7

Query Match          50.0%  Score 16; DB 1; Length 6;
Best Local Similarity 60.0%  Pred. NO. 2.5e+05;
Matches 3; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 LTIS 7
DB 2 LTLSN 6

RESULT 10
US-08-478-386A-46
; Sequence 46, Application US/08478386A
; Patent No. 5830462
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
; TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOCS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,386A
; FILING DATE: 07/JUN/1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Flagg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-114A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6031
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-478-386A-46

Query Match          50.0%  Score 16; DB 2; Length 6;
Best Local Similarity 75.0%  Pred. NO. 2.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTIS 6
DB 3 LTVS 6

RESULT 11
US-08-292-597-46
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; Sequence 46, Application US/08292597
; Patent No. 5834266
; GENERAL INFORMATION:
; APPLICANT: Gerald R. Crabtree
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: REGULATED Apoptosis
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOCS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,597
; FILING DATE: 18/AUG/1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Flagg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-138A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-292-597-46

Query Match          50.0%  Score 16; DB 2; Length 6;
Best Local Similarity 75.0%  Pred. NO. 2.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTIS 6
DB 3 LTVS 6

RESULT 12
US-08-388-653-46
; Sequence 46, Application US/08388653
; Patent No. 5869337
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
; TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,653
FILING DATE: 14-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,386
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Figg, E. Anthony
REGISTRATION NUMBER: 27,195
REFERENCE/DOCKET NUMBER: 2854-114A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-388-653-46

Query Match 50.0%; Score 16; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0;
Gaps 0;

QY 3 LTIS 6
DB 3 LTVS 6

RESULT 13
US-08-473-985-46
Sequence 46, Application US/08473985
Patent No. 5871753
GENERAL INFORMATION:
APPLICANT: Crabtree, Gerald R.
APPLICANT: Schreiber, Stuart L.
APPLICANT: Spencer, David M.
APPLICANT: Wandless, Thomas J.
APPLICANT: Belshaw, Peter
APPLICANT: Ho, Steffan
TITLE OF INVENTION: Regulated Transcription of Targeted Genes and
TITLE OF INVENTION: Other Biological Events
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Fiore
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,985
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/179,748
FILING DATE: 07-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,615
REFERENCE/DOCKET NUMBER: P-SU 5863

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-473-985-46

Query Match 50.0%; Score 16; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0;
Gaps 0;

QY 3 LTIS 6
DB 3 LTVS 6

RESULT 14
US-08-834-108-7
Sequence 7, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-834-108-7

Query Match 50.0%; Score 16; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0;
Gaps 0;

QY 3 LTIS 7
DB 2 LTLSN 6

RESULT 15

US-08-483-898-46
 : Sequence 46, Application US/08483898
 : Patent No. 5994333
 : GENERAL INFORMATION:
 : APPLICANT: Gerald R. Crabtree
 : APPLICANT: Schreiber, Stuart J.
 : APPLICANT: Spencer, David M.
 : APPLICANT: Wandless, Thomas J.
 : APPLICANT: Belshaw, Peter
 : TITLE OF INVENTION: Regulated Apoptosis
 : NUMBER OF SEQUENCES: 81
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: ARCAD Pharmaceuticals, Inc.
 : STREET: 26 Landsdowne Street
 : CITY: Cambridge
 : STATE: Massachusetts
 : COUNTRY: USA
 : ZIP: 02139
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC/DOS/MS/DOS
 : SOFTWARE: Patent in Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/483,898
 : FILING DATE: 07-JUN-1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/252,597
 : FILING DATE: 18-AUG-1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Figg, E. Anthony
 : REGISTRATION NUMBER: 27,195
 : REFERENCE/DOCKET NUMBER: 2054-108A
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (202) 783-6040
 : TELEFAX: (202) 783-6031
 : INFORMATION FOR SEQ ID NO: 46:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 6 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-483-898-46

Query Match 50.0%; Score 16; DB 2; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 3 LTVS 6
 DB 3 LTVS 6

Search completed: October 4, 2003, 12:50:33
 Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw mode:

Run on: October 4, 2003, 12:40:52 ; Search time 19.3333 Seconds
(without alignments' sec
34.920 Million cell updates/sec

Title: US-09-712-819C-5

Perfect score: 35

Sequence: 1 TQFTLTL: 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9618662 residues

Total number of hits satisfying chosen parameters: 455

Minimum DB seq length: 3

Maximum DB seq length: 7

Post-processing: Minimum Match 10%

Maximum Match 100%

Listing first 45 summations

Database :

1: PIR 756**

2: PIR1**

3: PIR2**

4: PIR3**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	37.1	6	PD0028	pev-kinin 2 - pera
2	12	34.3	5	A32516	cholecystokinin-5
3	12	34.3	5	PT0644	T-cell receptor be
4	12	34.3	7	B30127	phosphotransferase
5	12	34.3	7	PT0655	T-cell receptor be
6	11	31.4	4	140697	histin A - Citrob
7	11	31.4	7	E30608	Ig kappa chain V-I
8	10	28.6	6	PT0650	T-cell receptor be
9	10	28.6	7	S09366	globulin IV alpha
10	9	25.7	3	T13892	cytochrome-c oxida
11	9	25.7	5	E43364	flagellar protein
12	9	25.7	5	E60274	major protein anti
13	9	25.7	5	S69326	blood cell protein
14	9	25.7	5	S69237	surface protein te
15	9	25.7	6	A60986	N-formyl oligopept
16	9	25.7	6	B44510	hypothetical prote
17	9	25.7	6	A43766	28K ubiquitin-immu
18	9	25.7	6	I37263	Y protein - human
19	9	25.7	6	I65546	MHC H2-L antigen -
20	9	25.7	6	PT0587	T-cell receptor be
21	9	25.7	6	S29881	Na+/K+-exchanging
22	9	25.7	7	S25266	p1E protein - Esc
23	9	25.7	7	A25269	sex pheromone csm3
24	9	25.7	7	A30512	sex pheromone cCf1
25	9	25.7	7	PT0611	T-cell receptor be
26	9	22.9	4	PT0697	T-cell receptor be
27	8	22.9	5	I39964	ribosomal protein
28	8	22.9	5	I39966	ribosomal protein
29	8	22.9	5	I39965	ribosomal protein

ALIGNMENTS

RESULT 1

PD0028

C:Species: Penaeus vannamei (Penaeus vannamei) (fragment)

C>Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 19-May-2000

C/Accession: PD0028

R:Nieto, J.; Veelaert, D.; Derua, R.; Waelekens, E.; Cerstiaens, A.; Coats, G.; Devreese

Biochem. Biophys. Res. Commun. 248, 406-411, 1998.

A>Title: Identification of one tachykinin- and two kinin-related peptides in the brain

A/Reference number: PD0027; MJD:98342103; PMID:9475150

A/Accession: PD0028

A/Molecule type: protein

A/Residues: 1-6 <NIE>

C/Comment: This peptide belongs to myotropic neuropeptides.

Query Match 37.1%; Score 13; DB 2; Length 6;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFT 4

DB 1 DFS 3

RESULT 2

A32516

N:Alternates names: CCK-5

C:Species: Canis lupus familiaris (dog)

C/Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000

C/Accession: A32516

R:Shively, J.; Reeve Jr., J.R.; Bysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J

Am. J. Physiol. 252, G272-G275, 1987

A>Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and int

A/Reference number: A32516; MJD:87153871; PMID:3826354

A/Accession: A32516

A/Molecule type: protein

A/Residues: 1-5 <SHI>

C/Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecy

C/Superfamily: gastrin

C/Keywords: amidated carboxyl end; neuropeptide

P:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 34.3%; Score 12; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DF 3

DB 4 DF 5

fulicin - giant Af
T-cell receptor be
T-cell receptor be
27.5 kda structural
27.5K structural p
27.5K structural p
28.5K structural p
28K structural p
Phytosulphine alp
transferrin - bovi
Fc epsilon RIib -
T-cell receptor be
T-cell receptor be
seed protein ws-5
28K protein 5507 -
T-cell receptor be

5 2 A44692
5 2 PT0729
5 2 PT0590
5 2 G44817
5 2 I44817
5 2 E44817
5 2 A44817
5 2 A44817
5 2 A44817
5 3 CT0870
6 2 A19780
6 2 A46474
6 2 PT0637
6 2 PT0641
7 2 E61491
7 2 PS0254
7 2 PT0642

```

RESULT 3
PT0644
A:Title: receptor beta chain V-D-J region (111-13) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0644
J:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991.
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0644
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <PEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      34.3%; Score 12; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TDFT 4
Db      2 SSFT 5

RESULT 4
B39127
Phosphotransferase system enzyme II (EC 2.7.1.69) - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 08-Oct-1999
C:Accession: B39127
J:Hardesty, C.; Ferran, C.; DiRienzo, J.M.
J. Bacteriol. 173, 449-456, 1991.
A:Title: Plasmid-mediated sucrose metabolism in Escherichia coli: characterization of sd
xin.
A:Reference number: A39127; MUID:9110325; PMID:1846143
A:Accession: B39127
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-7 <HAR>
A:Cross-references: GB:M38416; NID:G155142; PIRN:AAA98418.1; PDB:G-55144
C:Keywords: phosphotransferase

Query Match      34.3%; Score 12; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DF 3
Db      2 DF 3

RESULT 5
PT0665
T-cell receptor beta chain V-D-J region (121-138) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0665
J:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991.
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0665
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-7 <PEE>
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      34.3%; Score 12; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DF 3
Db      2 DF 3

RESULT 6
PT0650
T-cell receptor beta chain V-D-J region (121-138) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0650
J:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991.
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0650
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <PEE>
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 DF 3
Db      1 BIVLT 5

RESULT 7
E30608
Ig kappa chain V-III region (Gag) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
C:Accession: E30608
J:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S.
J. Immunol. 142, 3158-3163, 1989.
A:Title: Structural and idiotypic characterization of the L chains of human IgM autoa
A:Reference number: A30601; MUID:89215279; PMID:2496163
A:Accession: E30608
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-7 <GON>
C:Keywords: heterotetramer; immunoglobulin

Query Match      31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 TD 2
Db      2 TD 3

RESULT 8
PT0650
T-cell receptor beta chain V-D-J region (121-138) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0650
J:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991.
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0650
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <PEE>
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 DF 3
Db      1 BIVLT 5

```

```

QY      2 DF 3
Db      6 DF 7

RESULT 6
I40697
Biotin A - Citrobacter freundii (fragment)
C:Species: Citrobacter freundii
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C:Accession: I40697
R:Shuan, D.; Campbell, A.
Gene 67, 203-211, 1988.
A:Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobac
A:Reference number: I40697; MUID:89006280; PMID:2971595
A:Accession: I40697
A:Status: preliminary; translated from GB/EMBL/DBSJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: GB:M21922; NID:G144434

Query Match      31.4%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TD 2
Db      2 TD 3

RESULT 7
E30608
Ig kappa chain V-III region (Gag) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
C:Accession: E30608
J:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S.
J. Immunol. 142, 3158-3163, 1989.
A:Title: Structural and idiotypic characterization of the L chains of human IgM autoa
A:Reference number: A30601; MUID:89215279; PMID:2496163
A:Accession: E30608
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-7 <GON>
C:Keywords: heterotetramer; immunoglobulin

Query Match      31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 DF 3
Db      1 BIVLT 5

RESULT 8
PT0650
T-cell receptor beta chain V-D-J region (121-138) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0650
J:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991.
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0650
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <PEE>
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 DF 3
Db      1 BIVLT 5

```

Query Match 28.6%; Score 10; DB 2; Length 6;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDTT 4
 : : :
 Db 3 SDAT 6

RESULT 9
 S09066
 globulin IV alpha subunit delta-1 chain, seed - cucurbit (fragments)
 N:Alternate names: IIS globulin alpha subunit delta-1 chain
 C:Species: Cucurbita sp. (Cucurbit)
 C:Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996
 C:Accession: S09066
 R:Ohmura, M.; Hara, I.; Matsubara, H.
 Plant Cell Physiol. 21, 157-167, 1980
 A:Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and
 A:Reference number: S09066
 A:Accession: S09066
 A:Molecule type: protein
 A:Residues: 1-6;7 <CRM>

Query Match 28.6%; Score 10; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DFTL 5
 : : :
 Db 3 DETI 6

RESULT 10
 T13892
 cytochrome-c oxidase (EC 1.9.3.1) chain I (imported) - river lamprey mitochondrion (frag
 C:Species: mitochondrion lampetra fluviatilis (river lamprey)
 C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C:Accession: T13892
 R:Delarbre, C.; Barriel, V.; Tillier, S.; Carvies, P.; Gachelin, G.
 Mol. Biol. Evol. 14, 807-813, 1997
 A:Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI
 A:Reference number: T13892
 A:Accession: T13892
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-3 <DEU>
 A:Cross-references: EMBL:Y09528; NID:G2340016; PIDD:CAA70721.1; PID:G4379123
 C:Genetics:
 A:Genome: mitochondrion
 A:Note: COI
 C:Keywords: mitochondrion; oxidoreductase

Query Match 25.7%; Score 9; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TL 5
 : : :
 Db 2 TL 3

RESULT 11
 T42364
 flagellar protein flir - Salmonella typhimurium (fragment)
 C:Species: Salmonella typhimurium
 C:Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 30-Sep-1993
 C:Accession: E42364
 R:Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.
 J. Bacteriol. 173, 3564-3572, 1991
 A:Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and seq
 A:Reference number: A42364; MUID:91258342; PMID:1646201
 A:Accession: E42364

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-5 <VOG>
 A:Cross-references: GB:K62404

Query Match 25.7%; Score 9; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TL 5
 : : :
 Db 3 TL 4

RESULT 12
 E60274
 major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
 C:Species: Mycobacterium tuberculosis
 C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
 C:Accession: E60274
 R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
 Infect. Immun. 59, 372-382, 1991
 A:Title: Isolation and partial characterization of major protein antigens in the cult
 A:Reference number: A60274; MUID:9109989; PMID:1899999
 A:Accession: E60274
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-5 <NAG>

Query Match 25.7%; Score 9; DB 2; Length 5;
 Best Local Similarity 25.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 FTLT 6
 : : :
 Db 2 YPIT 5

RESULT 13
 S68326
 blood cell protein B - Ascidia ceratodes (fragment)
 N:Alternate names: Abcp-B
 C:Species: Ascidia ceratodes
 C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jun-1999
 C:Accession: S68326
 R:Taylor, S.W.; Ross, M.M.; Waite, J.H.
 Arch. Biochem. Biophys. 324, 228-240, 1995
 A:Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from
 A:Reference number: S68325; MUID:96132650; PMID:8554314
 A:Accession: S68326
 A:Molecule type: protein
 A:Residues: 1-5 <TAY>
 P:2/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental
 P:4/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental

Query Match 25.7%; Score 9; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DF 3
 : : :
 Db 2 DY 2

RESULT 14
 S69237
 surface protein tetraabrachion heavy chain - Staphylothermus marinus (fragment)
 C:Species: Staphylothermus marinus
 C:Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
 C:Accession: S69237
 R:Peterson, J.; Nitsch, M.; Kuehlmoegen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; Eng
 J. Mol. Biol. 245, 385-401, 1995
 A:Title: Tetraabrachion: a filamentous archaeobacterial surface protein assembly of unu

A:Reference number: S69237; MUID:95139068; PMID:7837271
 A:Accession: S69237
 A:Molecule type: protein
 A:Residues: 1-5 <PE>
 A:Experimental source: strain F1, DSM 1639
 C:Keywords: cell wall; glycoprotein; heat-stable protein

Query Match 25.7% Score 9; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TD 5
 |
 |
 Db 2 TD 3

RESULT 15

A60986
 N-formyl oligopeptide - Escherichia coli (fragment)
 C:Species: Escherichia coli
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #ext_change 31-Dec-1993
 C:Accession: A60986
 R:Broom, M.P.; Mollor, D.M.; Chadwick, V.S.
 Experientia 45, 1097-1099, 1989
 A:Title: Purification and amino acid sequencing of naturally occurring N-formyl-methionyl
 A:Reference number: A60986; MUID:90092406; PMID:2689204
 A:Accession: A60986
 A:Molecule type: protein
 A:Residues: 1-6 <BRO>
 C:Comment: This hexapeptide was the longest of several N-formyl oligopeptides reported.
 P:1/Modified site: N-formylmethionine #status experimental

Query Match 25.7% Score 9; DB 2; Length 6;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FTL 5
 |
 |
 Db 3 FIL 5

Search completed: October 4, 2003, 12:49:37
 Job time : 20.3333 secs

GenCore version: 5.1.6
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OM protein - protein search, using sw mode:

Run on: October 4, 2003, 12:27:32 ; Search time 10 Seconds
(without alignments)
32,919 Million cell updates/sec

Title: US-09-712-819C-5
Perfect score: 35
Sequence: 1 TDFTLTI 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 0
Maximum DB seq length: ?

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : SwissProt_41*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	14	40.0	7	1 ALL7_CVDPO	P82159 Cydia pomonella
2	12	34.3	5	1 RE11_LITRU	P82070 Litoria rubella
3	11	31.4	5	1 B10A_CITFR	P13071 Citrobacter
4	11	31.4	5	1 RE31_LITRU	P82072 Litoria rubella
5	11	31.4	5	1 RE32_LITRU	P82073 Litoria rubella
6	10	28.6	5	1 E104_LITRU	P82100 Litoria rubella
7	9	25.7	7	1 CCF1_ENTPA	P20134 enterococci
8	9	25.7	7	1 CIA_ENTPA	P11932 enterococci
9	8	22.9	5	1 ALL3_CARMA	P81817 carcinus ma
10	8	22.9	5	1 PSK_DAUCA	P58261 daucus caro
11	8	22.9	5	1 RE2_LITRU	P82071 Litoria rubella
12	8	22.9	7	1 ALL2_CARMA	P81805 carcinus ma
13	8	22.9	7	1 ALL3_CARMA	P81806 carcinus ma
14	8	22.9	7	1 ALL4_CARMA	P81807 carcinus ma
15	8	22.9	7	1 ALL5_CARMA	P81808 carcinus ma
16	8	22.9	7	1 PAR_ASCSU	P31889 ascaris suu
17	7	20.0	4	1 RM01_YEAR	P36515 saccharomyc
18	7	20.0	6	1 FARP_MONEX	P41966 moniezia ex
19	7	20.0	6	1 LOK1_LOCM1	P41491 locusta mig
20	7	20.0	6	1 UN06_CLOPA	P81351 clostridium
21	7	20.0	7	1 FARI_NACRS	P83274 macrobrachi
22	7	20.0	7	1 FARI_PROCL	P38493 procambatus
23	7	20.0	7	1 FARI_PROCL	P38498 procambatus
24	7	20.0	7	1 FARI_PANRE	P41875 panagrellus
25	7	20.0	7	1 FARP_CALVC	P41866 caliphora
26	7	20.0	7	1 GFRP_MOUSE	P59025 mus musculu
27	7	20.0	7	1 IGAO_DACDE	P06294 dactylium d
28	6	17.1	3	1 LUXE_VIBFI	P24272 vibrio fisc
29	6	17.1	4	1 ACHI_ACHFU	P35904 achatina fu
30	6	17.1	4	1 FARI_HIRME	P42562 hirudo medi
31	6	17.1	4	1 FARI_HIRME	P42563 hirudo medi
32	6	17.1	4	1 FFAA_HIRME	P58705 anthop-leura
33	6	17.1	4	1 FLRF_HIRME	P42561 hirudo medi

34 6 17.1 4 1 FLRF_ANTEU P58707 anthop-leura
35 6 17.1 4 1 FLRF_MACMI P0162 macrocallis
36 6 17.1 4 1 FARI_ANTEU P58706 anthop-leura
37 6 17.1 4 1 OCP1_OCTWI P58648 octopus min
38 6 17.1 4 1 OCP3_OCTWI P58649 octopus min
39 6 17.1 5 1 E103_LITRU P82099 litoria rub
40 6 17.1 5 1 FARP_ARTTR P41853 artiposhti
41 6 17.1 5 1 PAR2_PARMA P81864 pardachitus
42 6 17.1 5 1 SUGA_ACHDO P19991 acheta dome
43 6 17.1 5 1 TPIS_CANFA P54714 canis famli
44 6 17.1 5 1 TRM3_ECOE P33973 escherichia
45 6 17.1 5 1 UC22_MAIZE P80628 zea mays (m

ALIGNMENTS

RESULT 1
ALL7_CVDPO STANDARD; PRT; 7 AA.
ID ALL7_CVDPO STANDARD; PRT; 7 AA.
AC P82159:
DT 30-MAY-2000 (Rel. 39, Created)
D: 30-MAY-2000 (Rel. 39, Last sequence update)
D: 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydia pomonella (Codling moth).
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
CC Tortricidae; Tortricidae; Olethreutinae; Cydia.
CX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Dave W., Johnson A.H., Maesire C.D., Scott A.G., Kinstanley D.,
RA Davey M., East P.D., Thorpe A.,
RA "Lepidopteran peptides of the allatostatin superfamily."
RE Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 873 MW; 672879CAB569350 CRC64;
Query Match 40.0%; Score 14; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 DFTL 5
DS 4 DEGL 7

RESULT 2
RE11_LITRU STANDARD; PRT; 5 AA.
ID RE11_LITRU STANDARD; PRT; 5 AA.
AC P82070:
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
CC Pelodyadinae; Litoria.
CX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.F., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RA "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";

```
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW:598; METHOD=FAE.
KW Amphibian defense peptide.
SC SEQUENCE 5 AA; 598 MW; 6DD9C9CB2A006C CRC64;

Query Match 34.4%; Score 12; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DF 3
DB 2 DF 3

RESULT 3
BIOA_CITER STANDARD; PRT; 5 AA.
AC P13071;
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenosyl-methionine-8-amino-7-oxononanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-9-oxononanoic acid aminotransferase) (DAPA
DE aminotransferase) (Fragment).
DE BCAA.
OS Citrobacter freundii.
CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC Enterobacteriaceae; Citrobacter.
EN NCBI_TaxID=546;
RX SEQUENCE FROM N.A.
RX MEDLINE=8936280; PubMed=2971595;
RA Shuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67-203-211(1988)
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC glutamonoate.
CC -!- COFACTOR: Pyridoxal phosphate.
CC -!- PATHWAY: Biotin biosynthesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
CC aminotransferases.

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or send an email to license@sib-sib.ch).

DR EMBL; Y21922; ; NOT ANNOTATED_CDS.
DR PIR; I40697; I40697.
DR InterPro; IPR003814; Aminotrans_3.
DR PROSITE; PS00602; AA_TRANSFER_CLASS_3; PARTIAL.
KW Biotin biosynthesis; Transferase; Aminotransferase;
KW Pyridoxal phosphate.
FT NON_TER 5
SC SEQUENCE 5 AA; 592 MW; 6AAAB1B1A6FC0900 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TD 2
DB 3 TD 4
```

```
RESULT 4
RE31_LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.1.
CS Litoria rubella (Desert tree frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
CC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinbrenner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAE.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 5
FT AMIDATION.
SC SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FT 4
DB 4 FT 5

RESULT 5
RE32_LITRU STANDARD; PRT; 5 AA.
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.2.
CS Litoria rubella (Desert tree frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
CC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RA "Peptides from the skin glands of the Australian buzzing tree frog
RA Litoria electrica. Comparison with the skin peptides from Litoria
RA rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide.
SC SEQUENCE 5 AA; 570 MW; 71A9C9CB62A00000 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 3 FT 4
1
4 FT 5

Db 3 TL 4

RESULT 6

E104 LITRU
ID E104 LITRU STANDARD; PRT; 5 AA.
AC P82100;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 4.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
CX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
TX TISSUE=Skin secretion;
Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog
Litoria electrica. Comparison with the skin peptides from Litoria
rubella.";
Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 5 AA; 616 MW; 61F2D1AC59AC0000 CRC64;
SQ SEQUENCE 5 AA; 616 MW; 61F2D1AC59AC0000 CRC64;

Query Match 28.6%; Score 10; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1.3e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DY 5 LTI 7
1
2 ITV 4

Db 0

RESULT 7

CCFL_ENTFA
ID CCFI_ENTFA STANDARD; PRT; 7 AA.
AC P20104;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CCF10.
OS Enterococcus faecalis (Streptococcus faecalis).
CC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
CX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
TX MEDLINE=89008313; PubMed=3139458;
Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
Adsit J.C., Dunn G.M., Suzuki A.;
"Structure of CCF10, a peptide sex pheromone which induces
conjugative transfer of the Streptococcus faecalis tetracycline
resistance plasmid, pCF10.";
J. Biol. Chem. 263:14574-14578(1988).
CC -1- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
HEMOLYSIN PLASMID PCF10.
PIR; A308:2; A30812.
KW Pheromone.
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 25.7%; Score 9; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 4 TL 5

RESULT 8

CIA_ENTFA
ID CIA_ENTFA STANDARD; PRT; 7 AA.
AC P11932;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
OS Enterococcus faecalis (Streptococcus faecalis).
CC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
CX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
TX MEDLINE=87005252; PubMed=3093276;
Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
White B.A., An F.Y., Clewell D.B., Suzuki A.;
"Isolation and structure of the Streptococcus faecalis sex pheromone,
CAM373.";
FEBS Lett. 206:69-72(1986).
CC -1- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DNCR CELLS
HARBORING CAM373.
CC -1- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR
SPECIFICITY OF PHEROMONES TO PLASMIDS.
CC -1- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
DR PIR; A25269; A25269.
KW Pheromone.
FT MOD_RES 7 AA; 734 MW; 75BD72059C05D80 CRC64;
SQ SEQUENCE 7 AA; 734 MW; 75BD72059C05D80 CRC64;

Query Match 25.7%; Score 9; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FTL 5
1
3 FTL 5

Db 0

RESULT 9

ALI4_CARMA
ID ALI4_CARMA STANDARD; PRT; 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 14.
OS Carcinus maenas (Common shore crab) (Great crab).
CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
CC Eubrachyura; Portunoidae; Portunidae; Carcinus.
CX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
TX TISSUE=Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
"Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 5 AA; 586 MW; 672879D5AB300300 CRC64;
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300300 CRC64;

Query Match 22.9%; Score 8; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 3 FTL 5
DB 3 FGL 5

RESULT 10
PSK_DAUCA STANDARD; PRT; 5 AA.
AC P58261; (Rel. 40, Created)
DT 16-OCT-2003 (Rel. 40, Last sequence update)
DT 16-OCT-2003 (Rel. 40, Last sequence update)
DT 16-OCT-2003 (Rel. 40, Last annotation update)
DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)]
DE Daucus carota (Carrot)
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Campanulids; Apiales; Apiaceae; Daucus.
ON NCBI_TaxID=4039;
RX [1]
RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.
RC STRAIN=cv. JS-Harumakigosun;
RC MEDLINE=2012743; PubMed=10750705;
RA Hanai H., Matsuro T., Yamamoto Y., Matsubayashi Y., Kobayashi T.,
RA Kanada H., Sakagami Y.;
RT "A secreted peptide growth factor, phytosulfokine, acting as a
RT stimulatory factor of carrot somatic embryo formation."
RL Plant Cell Physiol. 41:27-32(2000).
CC -1- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE
CC CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC
CC EMBRYOS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A
CC PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.
KW Growth factor; Sulfation.
FT PEPTIDE 1 4 PHYTOSULFOKINE-BETA.
FT MOD RES 1 1 SULFATION.
FT MOD RES 3 3 SULFATION.
SQ SEQUENCE 5 AA; 687 MW; 76C19B504B3C0000 CRC64;

Query Match 22.9%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 FT 4
DB 3 YT 4

RESULT 11
RE21_LITRU STANDARD; PRT; 5 AA.
AC P82071; (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 2.1.
OS Litoria rubella (Desert tree frog)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
ON NCBI_TaxID=104895;
RX [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RC Steinborner S.T., Wabnitz P.A., Waugh R.J., Howie J.H., Gao G.,
RA Tyler M.O., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians."
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic
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CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -1- MASS SPECTROMETRY: MW=626; METHCD=FAB.
KW Amphibian defense peptide.
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB1C3C0000 CRC64;

Query Match 22.9%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DF 3
DB 2 EF 3

RESULT 12
ALL2_CARMA STANDARD; PRT; 7 AA.
AC P81805;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 2.
OS Carcinus maenas (Common shore crab) (Green crab);
CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
CC Eubrachyura; Portunoidea; Portunidae; Carcinus.
ON NCBI_TaxID=6759;
RX [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RC MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 7 7 AMIDATION (POTENTIAL).
SQ SEQUENCE 7 AA; 770 MW; 672679CDB5DB70 CRC64;

Query Match 22.9%; Score 8; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.3e+35;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FTL 5
DB 5 FGL 7

RESULT 13
ALL3_CARMA STANDARD; PRT; 7 AA.
AC P81806;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 3.
OS Carcinus maenas (Common shore crab) (Green crab);
CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
CC Eubrachyura; Portunoidea; Portunidae; Carcinus.
ON NCBI_TaxID=6759;
RX [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RC MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
```

T allatostatin superfamily in the shore crab *Carcinus maenas*.";
 L Eur. J. Biochem. 250:727-734(1997).
 C -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 C -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 C Neuropeptide; Multigene family.
 KW MOD.RES 7 AA; 781 MW; 672879CCEB476420 CRC64;
 SQ SEQUENCE 7 AA; 781 MW; 672879CCEB476420 CRC64;

Query Match 22.9%; Score 8; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DY 3 FTU 5
 DB 5 FGL 7

RESULT 14

ALL4_CARMA STANDARD; PRT; 7 AA.
 D P81807;
 T 30-MAY-2000 (Rel. 39, Created)
 T 30-MAY-2000 (Rel. 39, Last sequence update)
 T 30-MAY-2000 (Rel. 39, Last annotation update)
 E Carcinustatin 4.
 OS Carcinus maenas (Common shore crab) (Green crab).
 C Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 C Eumalacostraca; Eucarida; Decapoda; Plecocyemata; Brachyura;
 C Eubrachyura; Portunoidae; Portunidae; Carcinus.
 NCBI_TaxID=6759;
 [1]
 N SEQUENCE.
 RP TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RC MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jarvis P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab *Carcinus maenas*.";
 RL Eur. J. Biochem. 250:727-734(1997).
 TC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC Neuropeptide; Multigene family.
 KW SEQUENCE 7 AA; 782 MW; 672879CCEB476420 CRC64;

Query Match 22.9%; Score 8; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DY 3 FTU 5
 DB 5 FGL 7

RESULT 15

ALL5_CARMA STANDARD; PRT; 7 AA.
 AC P81808;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 5.
 OS Carcinus maenas (Common shore crab) (Green crab).
 C Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 C Eumalacostraca; Eucarida; Decapoda; Plecocyemata; Brachyura;
 C Eubrachyura; Portunoidae; Portunidae; Carcinus.
 NCBI_TaxID=6759;
 [1]
 N SEQUENCE.
 RP TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RC MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jarvis P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab *Carcinus maenas*.";

RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Multigene family.
 FT MOD.RES 7 AA; 781 MW; 672879CCEB476420 CRC64;
 SQ SEQUENCE 7 AA; 781 MW; 672879CCEB476420 CRC64;

Query Match 22.9%; Score 8; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DY 3 FTU 5
 DB 5 FGL 7

Search completed: October 4, 2003, 12:46:01
 Job time: 11 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:40:19 ; Search time 43 Seconds
(without alignments)
37.633 Million cell updates/sec

Title: JS-09-712-819C-5
Perfect score: 35
Sequence: 1 TDFLTI 7

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 67

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 38
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mba.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_revert.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacterioph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	31.4	7	2	Q54248 streptomyce
2	10	28.6	7	2	O34028 sphingomona
3	9	25.7	7	2	O07354 synechococ
4	9	25.7	7	10	P82445 nicotiana
5	9	25.7	7	15	Q8JEB1 Q8JEB1 human immun
6	8	22.9	7	2	P70804 azotobacter
7	7	20.0	5	2	P83073 bacillus ce
8	7	20.0	7	2	O47C29 enterobacte
9	7	20.0	7	2	P72681 P72681: nocardia la
10	7	20.0	7	8	C98866 C98866 spinacia ol
11	6	17.1	5	13	P83308 P83308 gallus gal.
12	6	17.1	6	10	P82541 P82541 spiracia ol
13	6	17.1	7	2	C50556 C50556 actinobacil
14	6	17.1	7	2	Q8KRS9 Q8KRS9 enterobacte
15	6	17.1	7	4	O15903 O15903 homo sapien
16	6	17.1	7	6	Q28742 Q28742 oryctolagus

17	6	17.1	7	8	Q6MFY6 Q6MFY6 taraxacum (
18	6	17.1	7	10	O49223 O49223 glycine max
19	6	17.1	7	10	Q9C5B3 Q9C5B3 arabidopsis
20	6	17.1	7	11	Q8X3H6 Q8X3H6 rattus norv
21	6	17.1	7	11	Q63480 Q63480 rattus norv
22	6	17.1	7	11	O55184 O55184 rattus norv
23	6	17.1	7	12	Q9YQ10 Q9YQ10 transmissib
24	6	17.1	7	13	Q8J20 Q8J20 gallus gal
25	5	14.3	6	10	P82181 P82181 spinacia ol
26	5	14.3	6	10	P82182 P82182 spinacia ol
27	5	14.3	7	2	Q8KMS3 Q8KMS3 klebsiella
28	5	14.3	7	2	Q475C5 Q475C5 escherichia
29	5	14.3	7	8	Q95945 Q95945 saccharomyc
30	5	14.3	7	10	P93233 P93233 lycopersico
31	5	14.3	7	12	Q67113 Q67113 influenzavi
32	5	14.3	7	12	C65578 C65578 bovine hepi
33	5	14.3	7	13	O42564 O42564 fugu rubrip
34	5	14.3	7	15	Q07624 Q07624 rous sarcom
35	4	11.4	4	11	Q08433 Q08433 rattus sp.
36	4	11.4	7	2	Q8GJ12 Q8GJ12 borrelia bu
37	4	11.4	7	2	Q8GJ04 Q8GJ04 borrelia bu
38	4	11.4	7	2	Q8GL00 Q8GL00 borrelia bu
39	4	11.4	7	4	Q8NH7 Q8NH7 homo sapien
40	4	11.4	7	4	Q15897 Q15897 homo sapien
41	4	11.4	7	8	P92214 P92214 amblyopyrum
42	4	11.4	7	8	P92393 P92393 hordeum vul
43	4	11.4	7	8	P92403 P92403 lophopyrum
44	4	11.4	7	8	P92427 P92427 peridictyon
45	4	11.4	7	8	O99182 O99182 gnathochlebia

ALIGNMENTS

RESULT 1
Q54248
ID Q54248 PRELIMINARY; PRT; 7 AA.
AC Q54248
DT 0-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE RplO protein (Fragment).
GN RPL0.
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales.
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
PN [..]
PE SEQUENCE FROM N.A.
RC STRAIN=N2-3-11;
RX MEDLINE=20011291; PubMed=10542330;
RA Poehling S., Piepersberg W., Wehmeier U.F.;
RT "Analysis and regulation of the sec Y gene from Streptomyces griseus
N2-3-11 and interaction of the SecY protein with the SecA protein.";
RL Biochim. Biophys. Acta 1447:238-302(1999).
DR EMBL; X95915; CAA65160.1; ..
FT NON TER
SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A3 CRC64;

Query Match. 31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 8.3e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TLT 6
Db 2 TVT 4

RESULT 2
O34028
ID O34028 PRELIMINARY; PRT; 7 AA.
AC O34028
DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update;
 CE Catechol-2,3-dioxygenase (Fragment)).
 GN PHNE.
 OS Sphingomonas chondrodenis.
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
 CC Sphingomonadaceae; Sphingomonas.
 CC NCB:TaxID=56193;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D077;
 RA Kim Y.-C.;
 RL Submitted (FEB-1997) to the EXBL/GenBank/DBJ databases.
 DR EMBL: J08298; AAB56311.1; --
 KW Diorygenase.
 FT NON_TER
 SQ SEQUENCE 7 AA; 968 MW; 74452D1A699D460 CRC64;
 Query Match 28.6%; Score 10; DB 2; Length 7;
 Best Local Similarity 33.3%; Pred. NO. 8.3e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 5 LTI 7
 DB 3 MTV 5

RESULT 3
 007354 PRELIMINARY; PRT; 7 AA.
 ID 007354
 AC 007354;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created);
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update;
 DE NifK (Fragment)).
 GN NIFK.
 OS Synecococcus sp. (strain PCC 8801 / RP-1) (Cyanothace PCC 8801).
 CC Bacteria; Cyanobacteria; Chroococcales; Cyanothace.
 CC NCB:TaxID=4131;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RP-1;
 RA HUANG T.C., Lin R.P., Chu M.K., Chen H.M.;
 RX MEDLINE=99211861; PubMed=10217509;
 RT "Organization and expression of nitrogen-fixation genes in the aerobic
 nitrogen-fixing unicellular cyanobacterium Synecococcus sp. strain
 RP-1".
 RT Microbiology 145:743-753(1999).
 RL EMBL: AF003700; AAC35193.1; --
 FT NON_TER
 SQ SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;
 Query Match 25.7%; Score 9; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. NO. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 FTL 5
 DB 3 FDL 5

RESULT 4
 P82445 PRELIMINARY; PRT; 7 AA.
 ID P82445
 AC P82445;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created);
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update);
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update);
 DE 10 kDa cell wall protein (fragment).
 OS Nicotiana tabacum (common tobacco).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; Lamiids; Solanales; Solanaceae; Nicotiana.

OX NCB:TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojtaszek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 tobacco culture".
 RL Planta 210:0-0(2000).
 CC -- SUBCELLULAR LOCATION: CELL WALL.
 CC -- TISSUE SPECIFICITY: XYLEM.
 KW Cell wall.
 FT NON_TER
 SQ SEQUENCE 7 AA; 758 MW; 69D2C1E8e2D1B2A3 CRC64;
 Query Match 25.7%; Score 9; DB 10; Length 7;
 Best Local Similarity 33.3%; Pred. NO. 8.3e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 5 LTI 7
 DB 1 VTV 3

RESULT 5
 Q8JEB1 PRELIMINARY; PRT; 7 AA.
 ID Q8JEB1
 AC Q8JEB1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created);
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Truncated pol protein (Fragment).
 GN PCL.
 OS Human immunodeficiency virus 1.
 CC Viruses; Retroviruses; Retroviridae; Lentivirus.
 OX NCB:TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=4874;
 RA MEDLINE=22056123; PubMed=12060770;
 RA Beerwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
 RA Hoifmann C., Korn K., Selbig J.;
 RT "Diversity and complexity of HIV-1 drug resistance: A bioinformatics
 approach to predicting phenotype from genotype".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
 DR EMBL: AF347267; AAK32344.1; --
 FT NON_TER
 SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C7C0 CRC64;
 Query Match 25.7%; Score 9; DB 15; Length 7;
 Best Local Similarity 100.0%; Pred. NO. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 TLI 5
 DB 4 TLI 5

RESULT 6
 P70824 PRELIMINARY; PRT; 7 AA.
 ID P70824
 AC P70824;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update);
 DE Aigt protein (Fragment).
 GN ALGT.
 OS Azotobacter vinelandii.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 CC Pseudomonadaceae; Azotobacter.
 OX NCB:TaxID=354;
 RN [1]
 RP SEQUENCE FROM N.A.

STRAIN=E;
MEDLINE=96427318; PubMed=8930682;
Rehm B.H.A., Ertesvåg H., Valla S.;
RT "A new Azotobacter vinelandii manuronan C-5-epimerase gene (a-ge) is
part of an alg gene cluster physically organized in a manner similar
to that in Pseudomonas aeruginosa";
J. Bacteriol. 178:5884-5889(1996).
DR EMBL; X87973; CAA61230.1; -;
NON_TER 1
FT SEQUENCE 7 AA; 684 MW; 7185ASASAZDLAED0 CRC64;
SQ

Query Match 22.9%; Score 8; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 TI 7
|:
|:
2 TV 3
DB

RESULT 7
P83073 PRELIMINARY; PRT; 5 AA.
AC P83073
DT 01-OCT-2001 (TREMBLrel. 18, Created;
01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update;
DE 88 kDa protein (Fragment);
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1196;
RN [1]
SQ SEQUENCE 5 AA; 623 MW; 68C1AA336F00C00 CRC64;
RC STRAIN=NCIMB 11796;
Browne N., Dowds R.C.A.;
Submitted (JUL-2001) to the SWISS-PROT data bank.
NON_TER 5
FT SEQUENCE 5 AA; 623 MW; 68C1AA336F00C00 CRC64;
SQ

Query Match 20.0%; Score 7; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TD 2
|:
|:
4 TE 5
DB

RESULT 8
Q47029 PRELIMINARY; PRT; 7 AA.
AC Q47029;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
01-NOV-1996 (TREMBLrel. 01, Last sequence update;
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update;
DE Aad A1 protein (Fragment).
OS AAD A1.
OC Enterobacteriaceae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=550;
RN [1]
SQ SEQUENCE FROM N.A.
MEDLINE=94079349; PubMed=8257126;
Rafter P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.C.;
RT "Analysis of the aac(3)-Via gene encoding a novel 3-N-
acetyltransferase";
Antimicrob. Agents Chemother. 37:2074-2079(1993).
DR EMBL; M88012; AAA16193.1; -;
NON_TER 1
FT SEQUENCE 7 AA; 744 MW; 633862D2C321AC30 CRC64;
SQ

Query Match 20.0%; Score 7; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 50.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LT 6
|:
|:
1 IT 2
DB

RESULT 9
P72081 PRELIMINARY; PRT; 7 AA.
AC P72081;
DT 01-FEB-1997 (TREMBLrel. 02, Created;
01-FEB-1997 (TREMBLrel. 02, Last sequence update;
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 3'-methylcephem hydroxylase (Fragment).
GN CSFF.
OS Nocardia lactamdurans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
OX NCBI_TaxID=1913;
RN [1]
SQ SEQUENCE FROM N.A.
MEDLINE=96009872; PubMed=7557411;
Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.J., Martin J.F.,
Liras P.;
RT "Characterization of the cmcH genes of Nocardia lactamdurans and
RT Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem
O-carbamoyltransferase for cephamycin biosynthesis";
Gene 162:21-27(1995).
RL EMBL; Z21682; CAA79797.1; -;
DR NON_TER 1
FT SEQUENCE 7 AA; 746 MW; 75A1B2CDF1E691C0 CRC64;
SQ

Query Match 20.0%; Score 7; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TD 5
|:
|:
1 TM 2
DB

RESULT 10
Q98866 PRELIMINARY; PRT; 7 AA.
AC Q98866;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update;
DE Cytochrome b/f subunit IV (Fragment).
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
SQ SEQUENCE FROM N.A.
MEDLINE=86120353; PubMed=3031688;
Rijben-Mueller G., Hallick R.B., Ait J., Westhoff P., Herrmann R.G.;
RT "Spinach plastid genes coding for initiation factor IF-1, ribosomal
RT protein S11 and RNA polymerase alpha-subunit";
Nucleic Acids Res. 14:1029-1044(1986).
DR EMBL; X01496; CAA27215.1; -;
KN Chloroplast.
FT NON_TER 1
SQ SEQUENCE 7 AA; 907 MW; 644729D77409C420 CRC64;
SQ

Query Match 20.0%; Score 7; DB 8; Length 7;
Best Local Similarity 50.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DF 3
DB 1 NF 2

RESULT 11
P83308 PRELIMINARY; PRT; 5 AA.
AC P83308; 2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE PWRamide-like neuropeptide (LPLRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
[1]
SEQUENCE, AND SYNTHESIS.
RP TISSUE=Brain;
RC PubMed=613771;
RA Dockray G.J., Reeve C.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
RT antibodies to PWRamide";
RL Nature 365:328-330 (1993).
CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC -!- SIMILARITY: BELONGS TO THE FAPP (PWRFAMIDE RELATED PEPTIDES;
CC FAMILY.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 17.1%; Score 6; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 F 3
DB 5 F 5

RESULT 12
P82541 PRELIMINARY; PRT; 6 AA.
ID P82541
AC P82541; 2003 (TREMBlrel. 15, Created)
DT 01-OCT-2003 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
OS Spinacia oleracea (Spinach).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
NCBI_TaxID=3562;
[1]
SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP STRAIN=cv. ALVARO; TISSUE=Leaf;
RC MEDLINE=20435797; PubMed=10874039;
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT "The plastid ribosomal proteins: identification of all the proteins in
RT the small subunit of an organelle ribosome (chloroplast)";
RL J. Biol. Chem. 272:28455-28465 (2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
CC -!- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
CC -!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PL. S19 BETA
CC FORM IS THE MINOR BASIC FORM.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS 12 KDA.
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPI002222; Ribosomal_S19.

DR Pfam: PF00203; Ribosomal S19; PARTIAL.
DR PRINTS; PR00975; RIBOSOMALS19; PARTIAL.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 732 MW; 6333735A411C000 CRC64;

Query Match 17.1%; Score 6; DB 10; Length 6;
Best Local Similarity 25.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 TLT1 7
DB 1 TRSL 4

RESULT 13
OS556 PRELIMINARY; PRT; 7 AA.
ID OS556
AC OS556; 1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE GLYA (Fragment).
OS Actinobacillus actinomycetecombitans (Haemophilus
OC actinomycetecombitans;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
NCBI_TaxID=714;
[1]
SEQUENCE FROM N.A.
RP STRAIN=ATCC 33384;
RC MEDLINE=96355846; PubMed=9751884;
RA Kolodrubetz D., Spitznagel S. Jr., Wang R., Phillips L.H., Jacobs C.,
RA Kraig E.;
RT "cis Elements and trans factors are both important in strain-specific
RT regulation of the leukotoxin gene in Actinobacillus
OC actinomycetecombitans";
RL Infect. Immun. 64:3451-3460 (1996).
DE EMBL; U51862; AAB86721.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 832 MW; 6DCB42D76734042C CRC64;

Query Match 17.1%; Score 6; DB 2; Length 7;
Best Local Similarity 33.3%; Pred. No. 8.3e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 TLT1 7
DB 3 LPTV 5

RESULT 14
Q8KMS9 PRELIMINARY; PRT; 7 AA.
ID Q8KMS9
AC Q8KMS9; 2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Putative transposase (Fragment).
OS TNIA.
OC Enterobacter sp. CH2-4.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
NCBI_TaxID=143777;
[1]
SEQUENCE FROM N.A.
RP STRAIN=CH2-4;
RC MEDLINE=21604134; PubMed=11763242;
RA Mirdlin S.Z., Kholodii G.Y., Gorlenko Z.M., Mirakhina S.V.,
RA Mirakhin L.S., Kalyaeva E.S., Kopteva A.V., Petrova N.A.,
RA Yurieva O.V., Nikiforov V.S.;

RT "Mercury resistance transposons of Gram-negative environmental
bacteria and their classification."
Res. Microbiol. 152:811-822(2001).
OR EMBL; AC302778; CAC83038.1; -
RT NON TER
SQ SEQUENCE 7 AA; 966 MW; 737B1B:045DA9AC CRC64;

Query Match 17.1%; Score 6; DB 2; Length 7;
Best Local Similarity 100.0%; Pred.No. 8.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 F 3
|
|
DDB 1 F 1

RESULT 15
Q15903 PRELIMINARY; PRT; 7 AA.
ID Q15903
AC Q15903;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE (Clone XP727B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
(1)
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Cocibaugh M., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
arrayed cDNAs and cosmid libraries."
RRL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; U32082; AAA79931.1; -
FT NON TER
FT 7
SQ SEQUENCE 7 AA; 549 MW; 6B04C339CDD33D8C CRC64;

Query Match 17.1%; Score 6; DB 4; Length 7;
Best Local Similarity 100.0%; Pred.No. 8.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 F 3
|
|
DDB 4 F 4

Search completed: October 4, 2003, 12:48:32
Job time : 49 secs

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: October 4, 2003, 12:26:27 / Search time 51.6667 Seconds
(without alignments)
21.505 Million cell updates/sec

Title: US-09-712-819C-5
Perfect score: 35
Sequence: 1 TFFTLT 7
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158728573 residues
Total number of hits satisfying chosen parameters: 76613

Minimum DB seq length: 0
Maximum DB seq length: 7
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_13Jun03.*			
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24:	/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	85.7	7	20	AAV40738
2	30	85.7	7	21	AA130076
3	27	77.1	7	20	AAV40737
4	27	77.1	7	21	AA130075
5	26	74.3	7	20	AAV40736
6	26	74.3	7	21	AA130074
7	21	60.0	7	20	AAV14399
8	20	57.1	5	23	AA085454
9	20	57.1	6	19	AAW31467

10	19	54.3	5	9	AA1302200
11	19	54.3	6	20	AAV06456
12	19	54.3	6	21	AAV77738
13	19	54.3	6	22	AA130076
14	19	54.3	6	22	AA130075
15	19	54.3	6	22	AA130074
16	19	54.3	6	22	AA130073
17	19	54.3	6	22	AA130072
18	19	54.3	6	22	AA130071
19	19	54.3	6	22	AA130070
20	19	54.3	6	22	AA130069
21	19	54.3	6	22	AA130068
22	18	51.4	6	19	AAV75358
23	18	51.4	7	11	AAW09409
24	18	51.4	7	19	AAW58711
25	18	51.4	7	20	AAV14403
26	18	51.4	7	22	AA130070
27	17	48.6	4	23	AA130069
28	17	48.6	4	23	AA130068
29	17	48.6	5	21	AA130067
30	17	48.6	5	21	AA130066
31	17	48.6	5	21	AA130065
32	17	48.6	5	23	AA130064
33	17	48.6	5	24	AA130063
34	17	48.6	5	24	AA130062
35	17	48.6	6	20	AAV06532
36	17	48.6	6	20	AAV06531
37	17	48.6	6	21	AAV06530
38	17	48.6	6	22	AA130061
39	17	48.6	6	22	AA130060
40	17	48.6	6	22	AA130059
41	17	48.6	6	22	AA130058
42	17	48.6	6	22	AA130057
43	17	48.6	6	22	AA130056
44	17	48.6	6	23	AA130055
45	17	48.6	6	23	AA130054

ALIGNMENTS

RESULT 1
AAV40738
ID AAV40738 standard; peptide: 7 AA.
XX AC AAV40738;
XX DT 01-DEC-1999 (first entry)
XX DE S4 derivative #12, beta strand of scaffold protein structure.
XX KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
XX KW tumour; chemotherapeutic agent.
XX CS Synthetic.
XX PN EP347582-A1.
XX PD 06-OCT-1999.
XX PF 31-MAR-1998; 98EP-0870065.
XX PR 31-MAR-1998; 98EP-0870065.
XX PA (INNO-) INNOGENETICS NV.
XX PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX DR WPI; 1999-542958/46.
XX PT New scaffold protein, useful for stabilizing antigens used as vaccines
XX TT

PS Disclosure; Page 6; 105pp; English.

XX Sequences AAY40727-Y40748 are functionally equivalent derivatives of the
CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a
CC beta strand peptide which forms part of a beta sheet. Peptides
CC (AAY40601-Y40609) together form a single-chain scaffold protein which
CC contains at least 1 disulfide bond, contains less than 10% alpha helix
CC and contains at least 6 beta-strands. The scaffold protein is constructed
CC of beta strands S1-S6, and may also include beta strands A1-A3, or any
CC functionally equivalent derivative of these sequences. The beta strands
CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to
CC the next by hydrogen bonds, which generate a beta sandwich architecture.
CC If the additional beta strands A1-A3 are included in the structure the
CC scaffold is constructed of two beta sheets with the structures
CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each
CC other via amino acid loops, where at least one of the loops binds to a
CC receptor or antigen. The scaffold protein is used to stabilize antigens
CC or whole proteins such as receptors, or their fragments. It may be used
CC to bind two separate molecules. For example, one surface of the scaffold
CC may be bound to a protein which binds to a tumour antigen. This will
CC target the complex to tumour cells. Another surface may be bound to a
CC cytotoxic molecule or an autoimmune antibody which may then kill the
CC tumour cells. Therefore the scaffold protein may be used to target
CC chemotherapeutic agents to specific cells. It may also be used to
CC stabilize individual peptides in a peptide library and may be used in
CC diagnostic techniques, and to stabilize antigens used as vaccines.

XX SQ Sequence 7 AA;

Query Match 85.7%; Score 10; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFTLTI 7
DB 1 DFTLTI 6

RESULT 2
AAB30076

ID AAB30076 standard; Peptide; 7 AA.

XX AAB30076;

XX 09-FEB-2002 (first entry)

XX Scaffold protein SCA S4 peptide SEQ ID NO: 137.

XX Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
XX SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
XX diabetic retinopathy; atherosclerosis.

XX Synthetic.

XX WC20C060070-A1.

XX 12-OCT-2000.

XX 01-APR-1999; 99WC-EP02283.

XX 01-APR-1999; 99WC-EP02283.

XX (INNO-) INNOGENETICS NV.

XX Desmet J, Hufton S, Hoogenboom H, Sablon E;

XX WPI; 2003-665002/64.

XX Scaffold composed of single-chain polypeptide having beta sandwich
XX architecture carrying raw and randomized peptide sequences useful as
XX supporting framework and carrying antigen- or receptor binding
XX fragments.

PS Disclosure; Page 15; 68pp; English.

XX The present invention is concerned with producing scaffold proteins
CC based upon the human CTLA-4 SCA domain. These scaffold proteins can be
CC used as a scaffold to bind antigen- or receptor-binding fragments. These
CC can be used in the treatment of diseases such as cancer,
CC atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and
CC diabetic retinopathy. Sequences AAB29930-529939 were used in the
CC production of the proteins of the invention.

XX SQ Sequence 7 AA;

Query Match 85.7%; Score 10; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFTLTI 7
DB 1 DFTLTI 6

RESULT 3
AAY40737

ID AAY40737 standard; peptide; 7 AA.

XX AAY40737;

XX 01-DEC-1999 (first entry)

XX S4 derivative #11, beta strand of scaffold protein structure.

XX Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
XX tumour; chemotherapeutic agent.

XX Synthetic.

XX EP947582-A1.

XX 06-OCT-1999.

XX 31-MAR-1998; 98EP-0870065.

XX 31-MAR-1998; 98EP-0870065.

XX (INNO-) INNOGENETICS NV.

XX Desmet J, Hufton S, Hoogenboom H, Sablon E;

XX WPI; 1999-542958/46.

XX New scaffold protein, useful for stabilizing antigens used as vaccines
XX -

XX Disclosure; Page 6; 105pp; English.

XX Sequences AAY40727-Y40748 are functionally equivalent derivatives of the
CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a
CC beta strand peptide which forms part of a beta sheet. Peptides
CC (AAY40601-Y40609) together form a single-chain scaffold protein which
CC contains at least 1 disulfide bond, contains less than 10% alpha helix
CC and contains at least 6 beta-strands. The scaffold protein is constructed
CC of beta strands S1-S6, and may also include beta strands A1-A3, or any
CC functionally equivalent derivative of these sequences. The beta strands
CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to
CC the next by hydrogen bonds, which generate a beta sandwich architecture.
CC If the additional beta strands A1-A3 are included in the structure the
CC scaffold is constructed of two beta sheets, with the structures
CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each
CC other via amino acid loops, where at least one of the loops binds to a
CC receptor or antigen. The scaffold protein is used to stabilize antigens
CC or whole proteins such as receptors, or their fragments. It may be used
CC to bind two separate molecules. For example, one surface of the scaffold
CC may be bound to a protein which binds to a tumour antigen. This will

target the complex to tumour cells. Another surface may be bound to a cytotoxic molecule or an autoimmune antibody which may then kill the tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may also be used to stabilize individual peptides in a peptide library and may be used in diagnostic techniques, and to stabilize antigens used as vaccines.

XX Sequence 7 AA;

Query Match 77.1%; Score 27; DB 20; Length 7;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 3; Gaps 0;

QY 2 DFTLTI 7
Db 1 DVTLLI 6

RESULT 4
AAB30075
ID AAB30075 standard; Peptide; 7 AA.

XX AAB30075;

XX 09-FEB-2002 (first entry)

XX Scaffold protein SCA S4 peptide SEQ ID NO: 136.

XX Human; CRLA-4; scaffold protein; antigen-binding; receptor-binding;
XX SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
XX diabetic retinopathy; atherosclerosis.

XX Synthetic.

XX WO200060070-A1.

XX 12-OCT-2000.

XX 01-APR-1999; 99WC-EP02263.

XX 01-APR-1999; 99WC-EP02263.

XX (INNO-) INNOGENETICS NV.

XX Desmet C, Hufton S, Hoogenboom H, Sablon E;

XX WPI; 2000-665022/64.

XX Scaffold composed of single-chain polypeptide having beta sandwich
PT architecture carrying new and randomized peptide sequences useful as
PT supporting framework and carrying antigen- or receptor binding
PT fragments.

XX Disclosure; Page 15; 68pp; English.

XX The present invention is concerned with producing scaffold proteins
CC based upon the human CRLA-4 SCA domain. These scaffold proteins can be
CC used as a scaffold to bind antigen- or receptor-binding fragments. These
CC can be used in the treatment of diseases such as cancer,
CC atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and
CC diabetic retinopathy. Sequences AAB29930-529939 were used in the
CC production of the proteins of the invention.

XX Sequence 7 AA;

Query Match 77.1%; Score 27; DB 21; Length 7;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFTLTI 7
Db 1 DVTLLI 6

RESULT 5

XX AAY40736

XX ID AAY40736 standard; peptide; 7 AA.

XX AAY40736;

XX 01-DEC-1999 (first entry)

XX S4 derivative #10, beta strand of scaffold protein structure.

XX Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
KW tumour; chemotherapeutic agent.

XX Synthetic.

XX EP947582-A1.

XX 06-OCT-1999.

XX 31-MAR-1998; 98EP-0870065.

XX 31-MAR-1998; 98EP-0870065.

XX (INNO-) INNOGENETICS NV.

XX Desmet C, Hufton S, Hoogenboom H, Sablon E;

XX WPI; 1999-542958/46.

XX New scaffold protein, useful for stabilizing antigens used as vaccines
PT .

XX Disclosure; Page 6; 105pp; English.

XX Sequences AAY40727-Y40748 are functionally equivalent derivatives of the
CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a
CC beta strand peptide which forms part of a beta sheet. Peptides
CC (AAY40601-Y40609) together form a single-chain scaffold protein which
CC contains at least 1 disulfide bond, contains less than 10% alpha helix
CC and contains at least 6 beta-strands. The scaffold protein is constructed
CC of beta strands S1-S6, and may also include beta strands A1-A3, or any
CC functionally equivalent derivative of these sequences. The beta strands
CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to
CC the next by hydrogen bonds, which generate a beta sandwich architecture.
CC If the additional beta strands A1-A3 are included in the structure the
CC scaffold is constructed of two beta sheets, with the structures
CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each
CC other via amino acid loops, where at least one of the loops binds to a
CC receptor or antigen. The scaffold protein is used to stabilize antigens
CC or whole proteins such as receptors, or their fragments. It may be used
CC to bind two separate molecules. For example, one surface of the scaffold
CC may be bound to a protein which binds to a tumour antigen. This will
CC target the complex to tumour cells. Another surface may be bound to a
CC cytotoxic molecule or an autoimmune antibody which may then kill the
CC tumour cells. Therefore the scaffold protein may be used to target
CC chemotherapeutic agents to specific cells. It may also be used to
CC stabilize individual peptides in a peptide library and may be used in
CC diagnostic techniques, and to stabilize antigens used as vaccines.

XX Sequence 7 AA;

Query Match 74.3%; Score 26; DB 20; Length 7;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFTLTI 7
Db 1 DFTLSI 6

RESULT 6
AAB30074

ID AAB30074 standard; peptide; 7 AA.

XX
AC AAB30074;

XX
DT 09-FEB-2001 (first entry)

XX
DE Scaffold protein SCA S4 peptide SEQ ID NO: 135.

XX
DE Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;

XX
KW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;
KW diabetic retinopathy; atherosclerosis.

XX
OS Synthetic.

XX
PN WO20060070-A1.

XX
PD 12-OCT-2000.

XX
PP 01-APR-1999; 99AC-EP02283.

XX
PR 01-APR-1999; 99AC-EP02283.

XX
PA (INNO-) INNOGENETICS NV.

XX
PI Desmet J, Hufton S, Hoogenboom H, Sablon E;

XX
DR WPI; 2000-665002/64.

XX
PT Scaffold composed of single-chain polypeptide having beta sandwich
PT architecture carrying new and randomized peptide sequences useful as
PT supporting framework and carrying antigen- or receptor binding
PT fragments.

XX
PS Disclosure; Page 15; 58pp; English.

XX
CC The present invention is concerned with producing scaffold proteins
CC based upon the human CTLA-4 SCA domain. These scaffold proteins can be
CC used as a scaffold to bind antigen- or receptor-binding fragments. There
CC can be used in the treatment of diseases such as cancer,
CC atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and
CC diabetic retinopathy. Sequences AAB2930-529939 were used in the
CC production of the proteins of the invention.

XX
SQ Sequence 7 AA:

Query Match 74.3%; Score 26; DB 21; Length 7;

Best Local Similarity 83.3%; Pred. No. 9.3e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 DFTLT; 7

Db 1 DFTLS; 6

RESULT 7

AAV:4399

ID AAV14399 standard; peptide; 7 AA.

XX
AC AAV14399;

XX
DT 17-AUG-1999 (first entry)

XX
DE Peptide CDR-H1-7 (Y3F) derived from anti-HCV protease MAb 8D4.

XX
KW Complementarity determining region; CDR; monoclonal antibody; MAb;

XX
KW hepatitis C virus; HCV; protease; binding site.

XX
OS Synthetic.

XX
PN JP112786-A.

XX
PD 18-MAR-1999.

PF 29-OCT-1997; 97JP-0297451.

XX
PR 29-OCT-1997; 97JP-0297451.

XX
PA (NIHA) JAPAN ENERGY CORP.

XX
DR WPI; 1999-350322/30.

XX
PT Neutralized antibody partial peptide derived from hepatitis C virus
PT - useful for inhibiting hepatitis C virus (HCV) serine protease
PT activity

XX
PS Example 1; Page 24; 32pp; Japanese.

XX
CC This sequence corresponds to a peptide (CDR-H1-7; AAV14393) derived from
CC the sequence of the heavy chain variable region complementarity
CC determining region (CDR)-1 of the anti-hepatitis C virus (HCV) Ser/Thr
CC protease monoclonal antibody (MAb) 8D4 protein. The peptide has a ty-
CC to Phe amino acid substitution at position 3 compared to the CDR-H1-7
CC peptide. The invention relates to the use of partial peptides
CC (AAV14348-Y14353) from the MAb 8D4 for inhibiting HCV serine protease
CC activity.

XX
SQ Sequence 7 AA:

Query Match 60.0%; Score 21; DB 20; Length 7;

Best Local Similarity 80.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TDFTL; 5

Db 1 TDFVL; 5

RESULT 8

AAU85454

ID AAU85454 standard; Peptide; 5 AA.

XX
AC AAU85454;

XX
DT 21-MAY-2002 (first entry)

XX
DE Human colon specific polypeptide antibody binding site #31.

XX
KW Human; colon specific gene; CSG; cytostatic; metastasis;

XX
KW colon cancer staging; antibody binding site.

XX
OS Homo sapiens.

XX
PN WC200206515-A2.

XX
PD 24-JAN-2002.

XX
PF 17-JUL-2001; 2001WO-US22454.

XX
PR 17-JUL-2000; 2000US-0618596.

XX
PA (DIAD-) DIADEXUS INC.

XX
PI Macina RA, Sun Y;

XX
DR WPI; 2002-171815/22.

XX
PT Diagnosing, staging or monitoring colon cancer involves determining a
PT colon specific gene in cells, tissues or body fluids in patient, and
PT comparing it with levels of the gene from a normal human control -

XX
PS Disclosure; Page 21; 52pp; English.

XX
CC The invention relates to diagnosing the presence of colon cancer,
CC metastases of colon cancer, staging colon cancer, monitoring colon cancer
CC for the onset of metastasis or monitoring a change in stage of colon
CC cancer in a patient. The method involves determining a colon specific

gene (CSG) in cells, tissues or bodily fluids and comparing it with levels of CSG in cells, tissues or bodily fluids from a normal human control. Colon cancer can be treated by administering a molecule which down regulates the expression or activity of CSG. An immune response against a target cell expressing CSG can be induced by delivering an immunologically stimulatory amount of a CSG protein to a patient, so that an immune response is mounted. Therapeutic agents are useful for imaging colon cancer in a patient by administering an agent labeled with paramagnetic ions or a radioisotope to the patient. They are also useful for preventing the onset of colon cancer, and in diagnosis and treatment of the disease. Sequences AAU85424-AAU85502 represent human colon specific protein antibody binding sites used in the method of the invention.

Sequence 5 AA;
Query Match 57.1%; Score 20; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FTLT 6
|||
Db 2 FTLT 5

RESULT 9
AAW31467
ID AAW31467 standard; Protein; 6 AA.

XX AAC

XX AAC

XX AAC

XX AAC

XX AAC

XX AAC

XX AAC

XX AAC

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XX AAC

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XX AAC

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XX AAC

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XX AAC

XX AAC

XX AAC

XX AAC

CC which interacts with Gallip into a cell containing Gallip and identifying members of the library that interact with the target from activation of transcription. Such constructs are used to activate transcription in a cell, e.g. for controlling gene activity, particularly in gene therapy (e.g. recognizing a site close to a selected therapeutic gene).

CC Transcription can be activated without blocking other transcriptional activators. They probably act by interacting with a component of the RNA polymerase II holoenzyme, Gallip, the strongest known yeast activator, which provides a more sensitive assay allowing detection of even weak protein-protein interactions. Such activators do not create toxicity problems even when overexpressed.

Sequence 6 AA;

Query Match 57.1%; Score 20; DB 10; Length 6;
Best Local Similarity 80.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFLT 5
|||
Db 1 TDFLT 5

RESULT 10
AAP82200
ID AAP82200 standard; Protein; 5 AA.

XX AAC

XX AAC

XX AAC

XX AAC

XX AAC

XX AAC

XX AAC

XX AAC

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XX AAC

Specific example of pentapeptide of the general formula of AAP82-97. These peptides can be administered intravenously, topically or perorally to relieve the symptoms of psoriasis or schizophrenia. Amino acids at posns 2 and 3 can be any residue but Asp is preferred at posn 3. See also AAP82196-9.

Sequence 5 AA;

Query Match 54.3%; Score 19; DB 9; Length 5;
Best Local Similarity 75.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLT 4
|||
Db 2 TDFLT 5

AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW319053-W39076 are fragments used in an assay to determine novel transcriptional activators. The method involves the production of transcriptional activators comprising of a DNA-binding group and a 6-25 amino acid peptide that is covalently bonded to the DNA binding group and does not represent a fragment of a natural transcription activator. Protein-protein interactions are identified in the assay by fusing a DNA-binding domain to a library of DNA fragments and introducing this and a fusion of target protein and a polypeptide containing a region of Gal4

Example 1; Page 26; 55pp; English.

Lu X, Ftaahne M, Wu Y;

WPI; 1998-018502/02.

N-PSDB; AAV32565.

New transcriptional activator containing DNA binding domain bound to peptide - useful for controlling gene expression, especially in gene therapy, and in protein-protein interaction assays, does not inhibit other transcription activators

Example 1; Page 26; 55pp; English.

AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW319053-W39076 are fragments used in an assay to determine novel transcriptional activators. The method involves the production of transcriptional activators comprising of a DNA-binding group and a 6-25 amino acid peptide that is covalently bonded to the DNA binding group and does not represent a fragment of a natural transcription activator. Protein-protein interactions are identified in the assay by fusing a DNA-binding domain to a library of DNA fragments and introducing this and a fusion of target protein and a polypeptide containing a region of Gal4

Example 1; Page 26; 55pp; English.

AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW319053-W39076 are fragments used in an assay to determine novel transcriptional activators. The method involves the production of transcriptional activators comprising of a DNA-binding group and a 6-25 amino acid peptide that is covalently bonded to the DNA binding group and does not represent a fragment of a natural transcription activator. Protein-protein interactions are identified in the assay by fusing a DNA-binding domain to a library of DNA fragments and introducing this and a fusion of target protein and a polypeptide containing a region of Gal4

Example 1; Page 26; 55pp; English.

AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW319053-W39076 are fragments used in an assay to determine novel transcriptional activators. The method involves the production of transcriptional activators comprising of a DNA-binding group and a 6-25 amino acid peptide that is covalently bonded to the DNA binding group and does not represent a fragment of a natural transcription activator. Protein-protein interactions are identified in the assay by fusing a DNA-binding domain to a library of DNA fragments and introducing this and a fusion of target protein and a polypeptide containing a region of Gal4

Example 1; Page 26; 55pp; English.

AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW319053-W39076 are fragments used in an assay to determine novel transcriptional activators. The method involves the production of transcriptional activators comprising of a DNA-binding group and a 6-25 amino acid peptide that is covalently bonded to the DNA binding group and does not represent a fragment of a natural transcription activator. Protein-protein interactions are identified in the assay by fusing a DNA-binding domain to a library of DNA fragments and introducing this and a fusion of target protein and a polypeptide containing a region of Gal4

Example 1; Page 26; 55pp; English.

AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW319053-W39076 are fragments used in an assay to determine novel transcriptional activators. The method involves the production of transcriptional activators comprising of a DNA-binding group and a 6-25 amino acid peptide that is covalently bonded to the DNA binding group and does not represent a fragment of a natural transcription activator. Protein-protein interactions are identified in the assay by fusing a DNA-binding domain to a library of DNA fragments and introducing this and a fusion of target protein and a polypeptide containing a region of Gal4

Example 1; Page 26; 55pp; English.

AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW319053-W39076 are fragments used in an assay to determine novel transcriptional activators. The method involves the production of transcriptional activators comprising of a DNA-binding group and a 6-25 amino acid peptide that is covalently bonded to the DNA binding group and does not represent a fragment of a natural transcription activator. Protein-protein interactions are identified in the assay by fusing a DNA-binding domain to a library of DNA fragments and introducing this and a fusion of target protein and a polypeptide containing a region of Gal4

RESULT 11
AAVC6466
ID AAY06466 standard; Peptide; 6 AA.

XX AC AAY06466;
XX
DT 27-SEP-1999 (first entry)
XX
DE Epitope tag.
XX
KW Epitope tag; antibody engineering; yeast; surface display;
KW protein library; peptide library.
XX
OS Synthetic.
XX
PN WO9936560-A1.
XX
PD 22-JUL-1999.
XX
PF 20-JAN-1999; 99WC-US0158.
XX
PR 26-AUG-1998; 98US-0140084.
PR 20-JAN-1998; 98US-0009388.
XX
PA (UNCL) UNIV ILLINOIS FOUND.
XX
PI Boder ET, Kioke NC, Kranz DM, Shusta E, Wittrup KD;
XX
DR WPI: 1990-430619/36.
XX
PT Selecting proteins with enhanced phenotypic properties than
PT wild-type proteins, is useful for highly specific cancer diagnosis
PT and therapy
XX
PS Disclosure; Page 7; 116pp; English.

XX
CC This peptide comprises an epitope tag that can be used in
CC methods of the invention. The invention discloses a powerful new
CC system for engineering antibody affinity and specificity, by
CC constructing a microbial analogue of the mammalian system of a cell
CC repertoire. Antibodies are displayed on the surface of yeast cells
CC by genetic fusion with yeast cell wall proteins, especially
CC agglutinin proteins. After mutation, variants are selected on the
CC basis of improved binding characteristics with fluorescently
CC labeled targets. The selection method also identifies proteins
CC with enhanced phenotypic characteristics, proteins that are
CC displayed at higher levels, proteins that are secreted at higher
CC efficiency and proteins of improved stability.
XX
SQ Sequence 6 AA;

Query Match 54.3%; Score 19; DB 20; Length 6;
Best Local Similarity 80.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTL 5
DB 1 TDFYL 5

RESULT 12
AAY77708
ID AAY77708 standard; peptide; 6 AA.

XX AC AAY77708;
XX
DT 12-MAY-2000 (first entry)
XX
DE AJS peptide epitope.
XX
KW Cell surface receptor; luminescence; protein internalization;
KW drug discovery; screening assay; epitope; AJS.

XX OS Synthetic.
XX PN WO200003246-A2.
XX
PD 20-JAN-2000.
XX
PF 13-JUL-1999; 99WO-US-5870.
XX
PR 13-JUL-1998; 98US-0092671.
XX
PA (CELL-) CELLOMICS INC.
XX
PI Rubin RA, Giuliano KA, Gough A, Dunlay T;
XX
DR WPI: 2000-171170/15.
XX
PT Automated screening method for identifying compounds which induce cell
PT surface receptor internalization, useful for drug discovery -
XX
PS Example 6; Page 67; 148pp; English.
XX
CC The invention relates to a method for identifying compounds which
CC inhibit internalization of cell surface receptors. Provided are an array
CC of locations, each containing cells with a cell surface receptor
CC protein, that are treated with a test compound. The protein is
CC luminescently labeled or contacted with a luminescently labeled cell
CC before or after test compound treatment. Any luminescence produced is
CC converted into digital data and automatically analysed to determine if
CC the test compound induced the protein internalization. The novel method
CC is used to screen for compounds which modulate cell surface receptor
CC protein internalization, this can be used in drug discovery. To test
CC compound efficacy in living biological systems. The assay method is
CC automated and compact. It has high throughput and uses smaller volumes of
CC reagents and test compounds. Sequences AAY77704-718 represent examples of
CC peptide epitope tags used in the course of the invention.
XX
SQ Sequence 6 AA;

Query Match 54.3%; Score 19; DB 21; Length 6;
Best Local Similarity 80.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTL 5
DB 1 TDFYL 5

RESULT 13
AAE13076
ID AAE13076 standard; peptide; 6 AA.

XX AC AAE13076;

DT 28-JAN-2002 (first entry)

XX Epitope tag #4 used in yeast cell surface display of proteins.
XX Phenotypic property; yeast; cell wall protein; epitope tag.
XX Unidentified.

XX PN US6300065-B1.

XX PD 09-OCT-2001.

XX PF 26-AUG-1998; 98US-0140094.

XX PR 31-MAY-1996; 96US-018741P.

XX PR 30-MAY-1997; 97US-0866398.

XX PR 20-JAN-1998; 98US-0009398.

XX PA (UNCL) UNIV ILLINOIS FOUND.

XX Kieke MC, Wittrup KO, Boder ET, Kranz DM, Shusta E;
 XX WPI; 2001-656236/75.
 XX
 XX Selecting proteins, e.g. antibodies, with enhanced phenotypic
 PT properties relative to those of a wild-type comprises transforming
 PT yeast cells with a vector expressing a protein to be tested fused to a
 PT yeast cell wall protein -
 XX
 XX Disclosure; Column 5; 64pp; English.
 XX
 XX The present invention relates to a method for selecting proteins with
 CC enhanced phenotypic properties relative to those of a wild-type,
 CC comprises transforming yeast cells with a vector expressing a protein
 CC to be tested fused to a yeast cell wall protein. The method is
 CC particularly useful for selecting antibodies for improved affinity and
 CC specificity. The present sequence is an epitope tag which is used in
 CC yeast cell surface display of proteins.
 XX
 XX SQ Sequence 6 AA;

Query Match 54.3%; Score 19; DB 22; Length 6;
 Best Local Similarity 80.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : TDFTL 5
 : : :
 Db 1 TDFYL 5

RESULT 14
 AAM51422
 ID AAM51422 standard; peptide; 6 AA.

XX AAM51422;
 XX AC
 XX DT 06-JAN-2002 (first entry)
 XX DE Integrin activating peptide SEQ ID NO 1.
 XX DE

XX Integrin stimulant; vulnery; injury healing;
 XX postsurgical tissue recovery.

XX Unidentified.

XX JP2001213898-A.

XX 07-AUG-2001.

XX 31-JAN-2000; 2000JP-0522469.

XX 31-JAN-2000; 2000JP-0522469.

XX (HISM) HISAKITSU PHARM CO LTD.

XX WPI; 2001-629610/73.

XX An injury healing and postsurgical tissue recovering integrin
 PT activating peptide -

XX Claim 1; Page 3; 11pp; Japanese.

XX The invention relates to novel peptides with vulnery activity, useful
 CC for injury healing and postsurgical tissue recovery by acting as an
 CC integrin stimulant.

XX SQ Sequence 6 AA;

Query Match 54.3%; Score 19; DB 22; Length 6;
 Best Local Similarity 60.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 FTLTI 7
 : : : :
 Db 1 YTI TI 5

RESULT 15

AAB97355
 ID AAB97355 standard; peptide; 6 AA.

XX AAB97355;
 XX AC

XX 15-AUG-2001 (first entry)

XX A05 epitope used in dual labelled receptor construction.

XX Automated measurement; cell viability; epitope tag; luminescence;

XX G-protein coupled receptor; high content screen.

XX Synthetic.

XX WO200135072-A2.

XX 17-MAY-2001.

XX 09-NOV-2000; 2000WO-US0896.

XX 09-NOV-1999; 99US-0164353.

XX 15-JAN-2000; 2000US-0176504.

XX (CELL-) CELLONICS INC.

XX Ghosh RN, Debiasio R, Chen Y, Bellutta P, Giuliano K, Pasley CW;

XX WPI; 2001-329169/34.

XX Automated measurement of cell viability. Involves contacting cells with
 PT luminescent reporter molecule, imaging cells to get signals, converting
 PT signals into digital data and using data to measure viable cell -

XX Example 6; Page 52; 155pp; English.

XX This invention relates to a method for the automated measurement of cell
 CC viability. The method involves contacting cells with luminescent
 CC reporter molecules, imaging cells to get signals, and converting the
 CC signals into digital data which can be used as a measure of cell
 CC viability. Included in the invention is a computer readable storage
 CC medium comprising a programme which causes the method of the invention
 CC to be activated. The method is useful for cell state identification in
 CC cells. The method is also useful for drug discovery. An example of the
 CC invention relates to the use of inserted sequences and their ligands for
 CC high content screens incorporating dual labelled receptors. The present
 CC sequence represents an epitope tag used to label one end of a G-protein
 CC coupled receptor (GPCR). The intracellular and extracellular domains of
 CC the GPCR are distinctly labelled so that using the method of the
 CC invention the extent of internalisation of the receptor can be measured.

XX SQ Sequence 6 AA;

Query Match 54.3%; Score 19; DB 22; Length 6;

Best Local Similarity 80.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTL 5
 : : : :
 Db 1 TDFYL 5

Search completed: October 4, 2003, 12:45:23
 Job time : 52.6667 secs

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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:48:43 ; Search time 33.6667 seconds
(without alignments)
32.896 Million cell updates/sec

Title: US-09-712-819c-5
Perfect score: 35
Sequence: 1 TDFTL 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 segs, 158212981 residues

Total number of hits satisfying chosen parameters: 33362

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications MA:*

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/1/pubpaa/PC1_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/1/pubpaa/PC1US_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/1/pubpaa/PC1US_PUBCOMB.pep.*
- 8: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
- 9: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 13: /cgn2_6/prodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/1/pubpaa/US105_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/1/pubpaa/US10C_NEW_PUB.pep.*
- 17: /cgn2_6/prodata/1/pubpaa/US63_NEW_PUB.pep.*
- 18: /cgn2_6/prodata/1/pubpaa/US63_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	54.3	5	12	US-10-315-964A-394
2	19	54.3	5	12	US-10-317-251A-394
3	19	54.3	5	12	US-10-317-252A-394
4	19	54.3	6	12	US-10-315-964A-402
5	19	54.3	6	12	US-10-317-251A-402
6	19	54.3	6	12	US-10-317-252A-402
7	19	54.3	6	15	US-10-C83-815-4
8	18	51.4	6	14	US-10-156-822-59
9	17	48.6	5	11	US-09-788-066-107
10	17	48.6	5	11	US-09-788-066-109
11	17	48.6	5	12	US-10-348-504-132
12	17	48.6	5	12	US-10-407-123-76
13	17	48.6	6	10	US-09-770-102A-55
14	17	48.6	6	12	US-10-172-919-25
15	17	48.6	7	11	US-09-954-385-257

16	45.7	6	12	US-10-286-393-5	Sequence 5, Appl
17	45.7	7	9	US-09-832-723-69	Sequence 69, Appl
18	45.7	7	12	US-10-303-331-69	Sequence 91, Appl
19	45.7	7	14	US-10-086-100-93	Sequence 2, Appl
20	42.9	5	11	US-09-788-066-2	Sequence 3, Appl
21	42.9	5	12	US-10-286-186-3	Sequence 3, Appl
22	42.9	5	12	US-10-286-186-4	Sequence 4, Appl
23	42.9	5	12	US-10-214-796-21	Sequence 21, Appl
24	42.9	6	10	US-09-233-854-8	Sequence 8, Appl
25	42.9	6	11	US-09-930-586-8	Sequence 8, Appl
26	42.9	6	12	US-10-310-113-8	Sequence 8, Appl
27	42.9	6	15	US-10-105-933-39	Sequence 39, Appl
28	42.9	6	15	US-10-036-869-650	Sequence 650, Appl
29	42.9	6	15	US-10-293-417-8	Sequence 8, Appl
30	42.9	7	9	US-09-734-417-12	Sequence 12, Appl
31	42.9	7	11	US-09-884-456-27	Sequence 27, Appl
32	42.9	7	11	US-09-281-495-19	Sequence 19, Appl
33	42.9	7	12	US-10-052-578-172	Sequence 172, Appl
34	42.9	7	12	US-10-271-708-14	Sequence 14, Appl
35	42.9	7	12	US-10-053-520-172	Sequence 172, Appl
36	42.9	7	14	US-10-030-552A-4	Sequence 4, Appl
37	42.9	7	15	US-10-036-869-651	Sequence 651, Appl
38	42.9	7	15	US-10-036-869-653	Sequence 653, Appl
39	42.9	7	15	US-10-044-692-142	Sequence 142, Appl
40	42.9	7	15	US-10-804-866-11	Sequence 11, Appl
41	40.0	5	9	US-09-890-748-2203	Sequence 2203, Appl
42	40.0	5	11	US-10-214-796-18	Sequence 18, Appl
43	40.0	5	15	US-09-727-963A-24	Sequence 24, Appl
44	40.0	6	10		
45	40.0	6	10		

ALIGNMENTS

RESULT 1

US-10-315-964A-394
; Sequence 394, Application US/10315964A
; Publication No. US20030148956A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M3
; CURRENT APPLICATION NUMBER: US/10/315,964A
; CURRENT FILING DATE: 2003-04-01
; PRIOR FILING DATE: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/388,995
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 394
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized artificial peptide
US-10-315-964A-394

Query Match 54.3%; Score 19; DB 12; Length 5;

Best Local Similarity 80.0%; Pred. No. 5.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : TDFTL 5
| | | |
Db 1 TKFTL 5

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RESULT 2
US-10-317-251A-394
; Sequence 394, Application US/10317251A
; Publication No. US20030148957A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M2
; CURRENT APPLICATION NUMBER: US/10/317,251A
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 394
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized artificial peptide
US-10-317-251A-394

Query Match 54.3%; Score 19; DB 12; Length 5;
Best Local Similarity 80.0%; Pred. No. 5.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTL 5
DB 1 TKFTL 5

RESULT 3
US-10-317-252A-394
; Sequence 394, Application US/10317252A
; Publication No. US20030148958A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M
; CURRENT APPLICATION NUMBER: US/10/317,252A
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 394
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized artificial peptide
US-10-317-252A-394

Query Match 54.3%; Score 19; DB 12; Length 5;
Best Local Similarity 80.0%; Pred. No. 5.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTL 5
DB 1 TKFTL 5

RESULT 4
US-10-315-964A-402
; Sequence 402, Application US/10315964A
; Publication No. US20030148956A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M3
; CURRENT APPLICATION NUMBER: US/10/315,964A
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 402
; LENGTH: 6
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized artificial peptide
US-10-315-964A-402

Query Match 54.3%; Score 19; DB 12; Length 6;
Best Local Similarity 80.0%; Pred. No. 5.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTL 5
DB 2 TKFTL 6

RESULT 5
US-10-317-251A-402
; Sequence 402, Application US/10317251A
; Publication No. US20030148957A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M2
; CURRENT APPLICATION NUMBER: US/10/317,251A
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 402
; LENGTH: 6
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized artificial peptide
US-10-317-251A-402

Query Match 54.3%; Score 19; DB 12; Length 6;
Best Local Similarity 80.0%; Pred. No. 5.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TDFTL 5
DB 2 TKFTL 6
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US-10-317-251A-402

Query Match 54.3%; Score 19; DB 12; Length 6;
Best Local Similarity 80.0%; Pred. No. 5.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TDFTL 5
Db 2 TKFTL 6

RESULT 6

US-10-317-252A-402
; Sequence 402, Application US/10317252A
; Publication No. US20030148952A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M
; CURRENT APPLICATION NUMBER: US/10/317,252A
; CURRENT FILING DATE: 2003-03-31
; PRIOR FILING DATE: 2002-03-16
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-03-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 402
; LENGTH: 6
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized artificial peptide

US-10-317-252A-402

Query Match 54.3%; Score 19; DB 12; Length 6;
Best Local Similarity 80.0%; Pred. No. 5.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TDFTL 5
Db 2 TKFTL 6

RESULT 7

US-10-083-815-4
; Sequence 4, Application US/10083815
; Publication No. US20030026781A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Clevenger, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING
; TITLE OF INVENTION: ENDOGENOUS INHIBITOR OF ATP SYNTHASE, INCLUDING
; TITLE OF INVENTION: TREATMENT FOR DIABETES
; FILE REFERENCE: 660088.435C2
; CURRENT APPLICATION NUMBER: US/10/083,815
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Epitope tag

US-10-083-815-4

Query Match 54.3%; Score 19; DB 15; Length 6;
Best Local Similarity 80.0%; Pred. No. 5.2e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TDFTL 5
Db 2 TDFYL 5

RESULT 8

US-10-156-820-59
; Sequence 59, Application US/10156820
; Publication No. US20020150558A1
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; APPLICANT: Hong, Saw See
; APPLICANT: Karavan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/10/156,820
; CURRENT FILING DATE: 2002-06-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/01005
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 59
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phagotopo

US-10-156-820-59

Query Match 51.4%; Score 18; DB 14; Length 6;
Best Local Similarity 60.0%; Pred. No. 5.3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DFTLT 6
Db 2 NYTLT 6

RESULT 9

US-09-788-006-107
; Sequence 107, Application US/09788006
; Publication No. US20030036093A1
; GENERAL INFORMATION:
; APPLICANT: Floudas, Christopher A.
; APPLICANT: Klepeis, John L.
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets,
; TITLE OF INVENTION: Peptide tertiary Structures
; FILE REFERENCE: PC-0007
; CURRENT APPLICATION NUMBER: US/09/788,006
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Streptomyces griseus
; US-09-788-006-107

Query Match 48.8%; Score 17; DB 11; Length 5;
Best Local Similarity 75.0%; Pred. No. 5.3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FTTLT 6
Db 2 FTVT 5

SEQUENCE DESCRIPTION: SEQ ID NO: 76;
US-10-407-123-76

Query Match 48.6%; Score 17; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.3e+35;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFT 4
 |||
Db 1 DFT 3

RESULT 13

US-09-770-102A-55
Sequence 55, Application US/09770102A
Publication No. US20030197506A1
GENERAL INFORMATION:
APPLICANT: Cyclacel
TITLE OF INVENTION: Compositions and Methods for Monitoring the Modification of Modified Peptides
FILE REFERENCE: 10369/1062
CURRENT APPLICATION NUMBER: US/09/770.102A
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/179283
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn version 3.1
SEQ ID NO 55
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Tag peptide
NAME/KEY: PEPTIDE
LOCATION: (1)...(6)
OTHER INFORMATION: Tag peptide
US-09-770-102A-55

Query Match 48.6%; Score 17; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.3e+35;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TDF 3
 |||
Db 1 TDF 3

RESULT 14

US-10-172-919-25
Sequence 25, Application US/10172919
Publication No. US20030152947A1
GENERAL INFORMATION:
APPLICANT: CROSSMAN, DAVID C.
APPLICANT: DUFF, GORDON W.
APPLICANT: FRANCIS, SHEILA E.
APPLICANT: KORNMAN, KENNETH S.
APPLICANT: BARNETT, KATHERINE
TITLE OF INVENTION: METHODS FOR DETECTING AND TREATING THE EARLY ONSET OF AGING-RELATED CONDITIONS
FILE REFERENCE: MSA-025.01
CURRENT APPLICATION NUMBER: US/10/172.919
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/298,493
PRIOR FILING DATE: 2001-06-15
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Illustrative
OTHER INFORMATION: peptide

US-10-172-919-25

Query Match 48.6%; Score 17; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TDF 3
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Db 2 TDF 4

RESULT 15

US-09-954-385-257
Sequence 257, Application US/09954385
Publication No. US20030100467A1
GENERAL INFORMATION:
APPLICANT: Ahle, Wolfgang
APPLICANT: Baldwin, Toby L.
APPLICANT: Van Gastel, Franciscus J.C.
APPLICANT: Janssen, Gisele G.
APPLICANT: Murray, Christopher J.
APPLICANT: Wang, Huaming
APPLICANT: Winetzkv, Deborah S.
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
FILE REFERENCE: GC690
CURRENT APPLICATION NUMBER: US/09/954.385
CURRENT FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 433
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 257
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: binding peptide
US-09-954-385-257

Query Match 48.6%; Score 17; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDF 3
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Db 1 TDF 3

Search completed: October 4, 2003, 13:05:04
Job time: 34.6667 secs

GenCore version 5.1.6
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MM protein - protein search, using sw model

Run on: October 4, 2003, 12:42:47 : Search time 17 seconds
Without alignments:
17,472 Million cell updates/sec

Title: US-09-712-819C-5
Perfect score: 35
Sequence: 2 TDFTLTI 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42110958 residues

Total number of hits satisfying chosen parameters: 45738

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTCTJS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	54.3	6	4	US-09-140-084-4
2	19	54.3	6	4	US-09-724-297-4
3	19	54.3	7	3	US-08-916-441A-8
4	19	54.3	7	3	US-08-643-737-38
5	18	51.4	6	4	US-09-155-613A-59
6	17	48.6	5	1	US-08-405-23C-10
7	17	48.6	5	2	US-08-913-990-10
8	17	48.6	5	4	US-09-367-777-132
9	17	48.6	5	4	US-09-367-791A-76
10	17	48.6	6	4	US-09-233-857-7
11	17	48.6	7	1	US-08-136-743B-29
12	17	48.6	7	2	US-08-136-743B-30
13	17	48.6	7	1	US-08-136-743B-31
14	17	48.6	7	1	US-08-136-743B-32
15	17	48.6	7	1	US-08-405-23C-5
16	17	48.6	7	2	US-08-910-993-5
17	17	48.6	7	2	US-08-739-401A-6
18	17	48.6	7	5	PCT-US93-11703-72
19	16	45.7	5	1	US-08-180-209B-14
20	16	45.7	5	3	US-08-393-745-14
21	16	45.7	5	3	US-08-591-632-17
22	16	45.7	5	3	US-08-591-632-23
23	16	45.7	5	3	US-08-591-632-26
24	16	45.7	5	3	US-08-485-368-14
25	16	45.7	5	3	US-08-474-853-14
26	16	45.7	5	4	US-09-166-205B-14
27	16	45.7	5	4	US-09-611-451-17

28 16 45.7 5 4 US-09-611-451-23 Sequence 23, Appl
29 16 45.7 5 4 US-09-611-451-26 Sequence 26, Appl
30 16 45.7 5 5 PCT-US94-02623-14 Sequence 14, Appl
31 16 45.7 6 1 US-08-252-995D-7 Sequence 7, Appl
32 16 45.7 6 2 US-08-482-228-12C Sequence 12C, Appl
33 16 45.7 6 2 US-08-934-106-7 Sequence 7, Appl
34 16 45.7 6 3 US-08-482-528-13C Sequence 13C, Appl
35 16 45.7 7 1 US-08-136-743B-55 Sequence 55, Appl
36 16 45.7 7 1 US-08-096-946-5 Sequence 5, Appl
37 16 45.7 7 2 US-08-177-106A-7 Sequence 7, Appl
38 16 45.7 7 2 US-08-697-706-7 Sequence 7, Appl
39 16 45.7 7 3 US-09-040-216-28 Sequence 28, Appl
40 16 45.7 7 3 US-09-173-941-52 Sequence 52, Appl
41 16 45.7 7 5 PCT-US94-07329-5 Sequence 5, Appl
42 15 42.9 5 1 US-08-136-743B-63 Sequence 63, Appl
43 15 42.9 5 1 US-07-789-184-126 Sequence 126, Appl
44 15 42.9 5 1 US-08-475-263-126 Sequence 126, Appl
45 15 42.9 5 1 US-08-485-886-126 Sequence 126, Appl

ALIGNMENTS

RESULT 1

US-09-140-084-4
: Sequence 4, Application US/09140084A
: Patent No. 6300065
: GENERAL INFORMATION:
: APPLICANT: Kieke, et al.
: TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
: FILE REFERENCE: D6061CIP2
: CURRENT APPLICATION NUMBER: US/09/140,084A
: CURRENT FILING DATE: 1998-08-26
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 4
: LENGTH: 6
: TYPE: PRT
: ORGANISM: Unknown
: FEATURE:
: OTHER INFORMATION: Description of Unknown Organism:Epitope Tag
US-09-140-084-4

Query Match: 54.3%; Score 19; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. NC. 2.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 TDFTL 5
|||
Db 1 TDFTL 5

RESULT 2

US-09-724-297-4
: Sequence 4, Application US/09724297
: Patent No. 6423538
: GENERAL INFORMATION:
: APPLICANT: The Board of Trustees of the University of Illinois
: APPLICANT: Wittup, et al.
: TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
: FILE REFERENCE: 97-99C
: CURRENT APPLICATION NUMBER: US/09/724,297
: CURRENT FILING DATE: 2000-11-28
: PRIOR APPLICATION NUMBER: US 09/009,388
: PRIOR FILING DATE: 1998-01-20
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: Patentin version 3.0
: SEQ ID NO 4
: LENGTH: 6
: TYPE: PRT
: ORGANISM: unknown
: FEATURE:
: NAME/KEY: misc_feature

LOCATION: {}
OTHER INFORMATION: Epitope tag
US-09-724-297-4

Query Match 54.3%; Score 19; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFTLT 5
DB 1 DFTLT 5

RESULT 3
US-08-916-443A-8

Sequence 8, Application US/08916443A
Patent No. 6001986
GENERAL INFORMATION:
APPLICANT: Yeng Sig KIM
APPLICANT: Sun Chung PARK
APPLICANT: Seo Kyung OH
APPLICANT: Hyeul Lee
APPLICANT: Geong Woo CHO
APPLICANT: Chang H. CHUNG
TITLE OF INVENTION: Activital Proteins, Awarantin 1 and 2, from
TITLE OF INVENTION: Acanthosus Viridis, DNAs Encoding Therefrom
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3+ Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WordPerfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,443A
FILING DATE: 22 AUG 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 1942/18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-916-443A-8

Query Match 54.3%; Score 19; DB 3; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DFTLT 7
DB 2 DFTLT 7

RESULT 4
US-08-640-737-38

Sequence 38, Application US/08640737
Patent No. 6215044
GENERAL INFORMATION:

APPLICANT: ARROWSMITH, David A.
APPLICANT: HELLYER, Susan A.
APPLICANT: DE SILVA, Jacqueline
APPLICANT: WHITEMAN, Sally A.
TITLE OF INVENTION: Tomato Xyloglucan Endo-Transglycosylase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,737
FILING DATE: 06-MAY-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/52467
FILING DATE: 10-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9323225.4
FILING DATE: 10-NOV-1993
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: unknown
US-08-640-737-38

Query Match 54.3%; Score 19; DB 3; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DFTLT 6
DB 3 DFTLT 7

RESULT 5
US-09-155-613A-59

Sequence 59, Application US/09155613A
Patent No. 6420120
GENERAL INFORMATION:
APPLICANT: Boulanger, Pierre
APPLICANT: Hong, Saw See
APPLICANT: Karayan, Lucie
TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
FILE REFERENCE: 032751-036
CURRENT APPLICATION NUMBER: US/09/155,613A
CURRENT FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: PCT/FR98/00184
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: FR 97/01005
PRIOR FILING DATE: 1997-01-30
PRIOR APPLICATION NUMBER: FR 97/11166
PRIOR FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 98
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 59
LENGTH: 6
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Phagotome
US-09-155-613A-59

Query Match 51.4%; Score 18; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFTLT 6
DB 2 NVTLT 6

RESULT 6
US-08-405-230-10
; Sequence 10, Application US/08405230
; Patent No. 5707846
; GENERAL INFORMATION:
; APPLICANT: TANIGUCHI, Naoyuki
; APPLICANT: NISHIKAWA, Atsushi
; APPLICANT: YAMAGUCHI, No. 5707846cm1
; TITLE OF INVENTION: NOVEL N-ACETYLGLUCOSAMINYL TRANSFERASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,230
; FILING DATE: 16-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/110,736
; FILING DATE: 23-AUG-1993
; FILING DATE: 24-AUG-1992
; APPLICATION NUMBER: JP 4-245950
; FILING DATE: 16-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/110,736
; FILING DATE: 23-AUG-1993
; FILING DATE: 24-AUG-1992
; APPLICATION NUMBER: JP 4-245950
; FILING DATE: 16-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-237118
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 001560-215
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; NAME/KEY: Peptide
; LOCATION: 1..5
; OTHER INFORMATION: /note= "Amino acid sequence
; OTHER INFORMATION: encoded by nucleotides 1-15 of SEQ ID NO. 7."

US-08-405-230-10

Query Match 48.6%; Score 17; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDF 3
DB 2 TDF 4

RESULT 7

US-08-910-990-10
; Sequence 10, Application US/08910990
; Patent No. 5834284
; GENERAL INFORMATION:
; APPLICANT: TANIGUCHI, Naoyuki
; APPLICANT: NISHIKAWA, Atsushi
; APPLICANT: YAMAGUCHI, No. 5834284cm1
; TITLE OF INVENTION: NOVEL N-ACETYLGLUCOSAMINYL TRANSFERASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,990
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/405,230
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: US 08/110,736
; FILING DATE: 23-AUG-1993
; APPLICATION NUMBER: JP 4-245950
; FILING DATE: 24-AUG-1992
; APPLICATION NUMBER: JP 5-237118
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 001560-215
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; NAME/KEY: Peptide
; LOCATION: 1..5
; OTHER INFORMATION: /note= "Amino acid sequence
; OTHER INFORMATION: encoded by nucleotides 1-15 of SEQ ID NO. 7."

US-08-910-990-10

Query Match 48.6%; Score 17; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDF 3
DB 2 TDF 4

RESULT 8

US-09-367-777-132
; Sequence 132, Application US/09367777
; Patent No. 6562598
; GENERAL INFORMATION:
; APPLICANT: Himmelspach, Michele
; FILED: 1999-08-10

Falkner, Falko-Guenther
Eibl, Johann
Dornier, Friedrich
Schlokat, Uwe
TITLE OF INVENTION: Factor X Deletion Mutants
and Analogues Thereof
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/367,777
FILING DATE: 12-NOV-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AT A 336/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT93/00046
FILING DATE: 27-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 20695D-000730US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-09-367-777-132

Query Match: 48.6%; Score 17; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFT 4
DB 1 DFT 3

RESULT 9
US-09-367-791A-76
Sequence 76, Application US/09367791A
Patent No. 6573071
GENERAL INFORMATION:
APPLICANT: Himmelspach, Michele
Schlokat, Uwe
Dornier, Friedrich
Fisch, Andreas
Eibl, Johann
TITLE OF INVENTION: Factor X Analogues With
a Modified Protease Cleavage Site
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/367,791A
FILING DATE: 12-NOV-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AT A 335/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00045
FILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,471
REFERENCE/DOCKET NUMBER: 20695D-000730US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-09-367-791A-76

Query Match: 48.6%; Score 17; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFT 4
DB 1 DFT 3

RESULT 10
US-09-233-857-7
Sequence 7, Application US/09233857
Patent No. 6495353
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
Plowman, Peter
TITLE OF INVENTION: HUMAN ORTHOLOGUES OF WART
FILE REFERENCE: 239/251
CURRENT APPLICATION NUMBER: US/09/233,857
CURRENT FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: USSN 60/372,023
EARLIER FILING DATE: 1998-01-21
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 6
TYPE: PPT
ORGANISM: HUMAN
US-09-233-857-7

Query Match: 48.6%; Score 17; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFT 3
DB 3 DFT 5

RESULT 11

US-08-136-743B-29

Sequence 29, Application US/08136743B

Patent No. 5459063

GENERAL INFORMATION:

APPLICANT: Barry S. Cooperman, Harvey Rubin,

APPLICANT: Jerome Salem, and Alison L. Fisher

TITLE OF INVENTION: "Plasmodium falciparum Ribonu-

TITLE OF INVENTION: cleotide Reductase, DNA Sequences Therefor and Peptide Inhibi-

TITLE OF INVENTION: Thereof"

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSEE: The University of Pennsylvania

STREET: Suite 330

STREET: 3700 Market Street

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19104-3246

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/136,743B

FILING DATE: 10/14/93

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 3957-10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: No. 5459063e

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-136-743B-29

Query Match 48.6%; Score 17; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDF 3

Db 5 TDF 7

RESULT 12

US-08-136-743B-30

Sequence 30, Application US/08136743B

Patent No. 5459063

GENERAL INFORMATION:

APPLICANT: Barry S. Cooperman, Harvey Rubin,

APPLICANT: Jerome Salem, and Alison L. Fisher

TITLE OF INVENTION: "Plasmodium falciparum Ribonu-

TITLE OF INVENTION: cleotide Reductase, DNA Sequences Therefor and Peptide Inhibi-

TITLE OF INVENTION: Thereof"

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSEE: The University of Pennsylvania

STREET: Suite 330

STREET: 3700 Market Street

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19104-3246

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

Query Match: 48.6%; Score 17; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDF 3
|||
Db 5 TDF 7

RESULT 14
US-08-136-743B-32
Sequence 32, Application US/08136743B
Patent No. 5459663
GENERAL INFORMATION:
APPLICANT: Barry S. Cooperman, Harvey Rubin,
APPLICANT: Jerome Salem, and Alison L. Fisher
TITLE OF INVENTION: "Plasmodium falciparum Ribonu-
TITLE OF INVENTION: cletotide Reductase, DNA Sequences Thereof and Peptide Inhibi-
TITLE OF INVENTION: Thereof"
NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:
ADDRESSEE: The University of Pennsylvania
STREET: Suite 330
STREET: 3700 Market Street
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19134-3246

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,743B
FILING DATE: 12/14/93
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 3957-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5459063e

INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-136-743B-32

Query Match: 48.6%; Score 17; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDF 3
|||
Db 5 TDF 7

RESULT 15
US-08-405-230-5
Sequence 5, Application US/08405230
Patent No. 5707846
GENERAL INFORMATION:
APPLICANT: TANIGUCHI, Naoyuki
APPLICANT: NISHIKAWA, Atsushi
APPLICANT: YAMAGUCHI, No. 5707846cm1
TITLE OF INVENTION: NOVEL N-ACETYLGLUCOSAMINYL TRANSFERASE
TITLE OF INVENTION: GENE CODING THEREFOR AND PROCESS FOR PRODUCTION THEREOF
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,230
FILING DATE: 16-MAR-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/110,736
FILING DATE: 23-AUG-1993
APPLICATION NUMBER: JP 4-24595C
FILING DATE: 24-AUG-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-237118
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Peury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 00:560-215

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-405-230-5

Query Match: 48.6%; Score 17; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TDF 3
|||
Db 2 TDF 4

Search completed: October 4, 2003, 12:50:34
Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:40:52 ; Search time :9.3333 Seconds
(without alignments)
34.820 Million cell updates/sec

Title: US-09-712-819c-6
Perfect score: 33
Sequence: 1: PTLKISR 7
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 293308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 456

Minimum DB seq length: 0
Maximum DB seq length: 7
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	15	45.5	7	2	S19630	ribosomal protein
2	13	39.4	7	2	A28709	phosphonoacetaldehy
3	12	36.4	5	2	T14910	hypothetical prote
4	11	33.3	5	2	PT0644	T-cell receptor be
5	10	30.3	7	2	PS0254	18K protein 5507 -
6	9	27.3	3	3	T13892	cytochrome-c oxida
7	9	27.3	4	2	I40604	endoglucanase F -
8	9	27.3	4	2	T46627	hypothetical prote
9	9	27.3	5	2	A60521	glycogen phosphory
10	9	27.3	5	2	E42364	flagellar protein
11	9	27.3	5	2	A43555	alkanal monooxygen
12	9	27.3	5	2	S11127	phosphoprotein, to
13	9	27.3	5	2	PT0525	T-cell receptor be
14	9	27.3	5	2	PT0577	T-cell receptor be
15	9	27.3	5	2	PT0565	T-cell receptor be
16	9	27.3	5	2	PT0700	T-cell receptor be
17	9	27.3	5	2	S62237	surface protein te
18	9	27.3	6	2	A65866	N-formyl oligopept
19	9	27.3	6	2	A43766	28K ubiquitin-immu
20	9	27.3	6	2	I37263	Y protein - human
21	9	27.3	6	2	B26206	alpha-1,4-glucan-p
22	9	27.3	6	2	T65546	MHC H2-L antigen
23	9	27.3	6	2	PT0518	T-cell receptor be
24	9	27.3	6	2	PT0662	T-cell receptor be
25	9	27.3	6	2	I49424	cytotoxic T-lympho
26	9	27.3	7	2	GN0859	peptidyl-dipeptida
27	9	27.3	7	2	A15198	choline oxidase (E
28	9	27.3	7	2	B30127	phosphotransferase
29	9	27.3	7	2	S25266	pi1b protein - Esc

sex pheromone CAM3
sex pheromone CCF:
omega-g-lutidine 1,
ribosomal protein
glycoprotein compo
DNA topoisomerase
T-cell receptor be
glutathione S-tran
major fat-globule
pullulanase (EC 3,
globulin IV alpha
hypothetical prote
ribosomal protein
ribosomal protein
ribosomal protein
R-phycocerythrin al

ALIGNMENTS

RESULT 1

S19630
ribosomal protein L30 - Streptomyces griseus (fragment)
C:Species: Streptomyces griseus
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 06-Jun-1997
C:Accession: S19630
R:Ochi, K.

Int. J. Syst. Bacteriol. 42, 144-150, 1992
A:Title: Electrophoretic heterogeneity of ribosomal protein AT-L30 among actinomycete
A:Reference number: S19630; MCLD:92144363; PMID:1736952
A:Accession: S19630
A:Molecule type: protein
A:Residues: 1-7 <OCH>

A:Experimental source: strain IFO 13189
C:Superfamily: Escherichia coli ribosomal protein L30
C:Keywords: protein biosynthesis; ribosome

Query Match 45.5%; Score 15; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.9e-05;
Matches 3; Conservative 2; Mismatches 0; Indels 3; Gaps 0;

Cy 3 LKISR 7

Db 3 LKITQ 7

RESULT 2

A28709
phosphonoacetaldehyde hydrolase - Bacillus cereus (fragment)
C:Species: Bacillus cereus

C:Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993
R:Olson, D.B., Hepburn, T.W., Moos, M., Mariano, P.S., Dunaway-Mariano, D.
Biochemistry 27, 2229-2234, 1988

A:Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Evidenc
due.
A:Reference number: A28709; MCLD:88241058; PMID:3132206
A:Accession: A28709
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <OLS>

Query Match 39.4%; Score 13; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 3 LKI 5

Db 1 LKI 3

RESULT 3

T14910
 hypothetical protein - parsley
 C:Species: Petroselinum crispum (parsley)
 C:Date: 20-Sep-1993 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
 C:Accession: F14910
 R:Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
 Mol. Gen. Genet. 257, 595-605, 1998
 A:Title: CPRP4a, a novel plant bZIP protein of the CPRF family: comparative analysis of
 A:Reference number: Z18261; MUID:982659-8; PMID:9604882
 A:Accession: T14910
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-5 <KRR>
 A:Cross-references: EMBL:Y10810; MUD:G3336904; PIDN:CAA71769.1; PID:G3336905
 A:Experimental source: ssp. Hamburger Schnitt

Query Match 36.4%; Score 12; DB 2; Length 5;
 Best Local Similarity 56.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISR 7
 |||
 Db 2 VSR 4

RESULT 4
 PT0644
 T-cell receptor beta chain V-D-J region (11-16) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0644
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <FEF>
 A:Experimental source: newborn thymus, strain B6J/c
 C:Keywords: T-cell receptor

Query Match 33.3%; Score 11; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
 |||
 Db 4 FT 5

RESULT 5
 PS0254
 18K protein 55C7 - rice (strain Nihonbare) (fragment)
 C:Species: Oryza sativa (rice)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
 C:Accession: PS0254
 R:Tsugita, A.
 submitted to JIPID, April 1993
 A:Reference number: PS0206
 A:Accession: PS0254
 A:Molecule type: protein
 A:Residues: 1-7 <TSU>
 A:Experimental source: leaf, chloroplast, strain Nihonbare
 A:Note: molecular weight 18K, pI 4.4

Query Match 30.3%; Score 10; DB 2; Length 7;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 LK-SR 7
 |||
 Db 1 LK-SR 5

RESULT 6
 T13892
 cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (f
 C:Species: mitochondrion Lampetra fluviatilis (river lamprey)
 C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C:Accession: T13892
 R:Delarbre, C.; Barriel, V.; Tillier, S.; Jarvies, P.; Gachelin, G.
 Mol. Biol. Evol. 14, 807-813, 1997
 A:Title: The main features of the craniate mitochondrial DNA between the ND1 and the
 A:Reference number: Z17775; MUID:97398704; PMID:9254918
 A:Accession: T13892
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-3
 A:Cross-references: EMBL:Y03528; MUD:G2340016; PIDN:CAA70721.1; PID:G4379123
 C:Genetics:
 A:Genome: mitochondrion
 A:Note: COI
 C:Keywords: mitochondrion; oxidoreductase

Query Match 27.3%; Score 9; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
 |||
 Db 2 TL 3

RESULT 7
 I40804
 endoglucanase F - Clostridium thermocellum (fragment)
 C:Species: Clostridium thermocellum
 C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Aug-1996
 C:Accession: I40804
 R:Mishra, S.; Beguin, P.; Aubert, J.
 J. Bacteriol. 173, 80-85, 1991
 A:Title: Transcription of clostridium thermocellum endoglucanase genes cef and celd
 A:Reference number: I40804; MUID:91100322; PMID:1987137
 A:Accession: I40804
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-4 <RES>
 A:Cross-references: GB:M64363; MUD:G144771
 C:Genetics:
 A:Gene: cef
 A:Start codon: TTG

Query Match 27.3%; Score 9; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KI 5
 |||
 Db 3 KI 4

RESULT 8
 T4627
 hypothetical protein c4 - loblolly pine
 C:Species: Pinus taeda (loblolly pine)
 C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
 C:Accession: T4627
 R:Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
 submitted to the EMBL Data Library, July 1995
 A:Description: Cloning of a chitinase homolog which lacks chitin binding sites and is
 A:Reference number: Z33105
 A:Accession: T4627
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-4 <CHA>

A:Cross-references: EMBL:U11309; NID:G974285; PID:G974202
 A:Experimental source: strain s6PT2xs6PT3; 8 month seedlings

Query Match 27.3%; Score 9; DB 2; Length 4;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LK 5
 |
 Db 1 MKL 3

RESULT 9

A60521
 glycogen phosphorylase (EC 2.4.1.11; muscle - mullet (Liza ramada) (fragment)
 N:Alternate names: glycogen phosphorylase b
 C:Species: liza ramada
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
 C:Accession: A60521
 R:Bonamusa, L.; Baanante, I.V.
 Comp. Biochem. Physiol. B 95, 295-301, 1990
 A:Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle
 A:Reference number: A60521; MUID:90227907; PMID:2109663
 A:Accession: A60521
 A:Molecule type: protein
 A:Superfamily: phosphorylase
 C:Keywords: glycosyltransferase; hexosyltransferase; phosphorylase
 F:3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experiment

Query Match 27.3%; Score 9; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KIS 6
 |
 Db 1 QIS 3

RESULT 10

E42364
 flagellar protein flir - Salmonella typhimurium (fragment)
 C:Species: Salmonella typhimurium
 C:Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 30-Sep-1993
 C:Accession: E42364
 R:Vogler, A.P.; Homma, Y.; Irikura, V.M.; Macnab, R.M.
 J. Bacteriol. 173, 3564-3572, 1991
 A:Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and secretion
 A:Reference number: A42364; MUID:91259342; PMID:164620
 A:Accession: E42364
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-5 <VOG>
 A:Cross-references: GB:V62408

Query Match 27.3%; Score 9; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TL 3
 |
 Db 3 TL 4

RESULT 11

A44955
 alkalal monooxygenase (FMN-linked) (EC 1.1.4.14.3) alpha chain - Vibrio harveyi (fragment)
 C:Species: Vibrio harveyi
 C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 25-May-2000
 C:Accession: A44955
 R:Paquatte, O.; Tu, S.C.
 Photochem. Photobiol. 50, 817-825, 1989
 A:Title: Chemical modification and characterization of the alpha cysteine 106 at the vib

A:Reference number: A44955; MUID:90175730; PMID:2626493
 A:Accession: A44955
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-5 <PAQ>
 C:Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match 27.3%; Score 9; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ISR 7
 |
 Db 3 IXR 5

RESULT 12

S11127
 phosphoprotein, bone - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000
 C:Accession: S11127; S11128
 R:Mikuni-Takagaki, Y.; Glincher, M.J.
 Biochem. J. 268, 585-591, 1990
 A:Title: Post-translational processing of chicken bone phosphoproteins. Identification
 A:Reference number: S11127; MUID:90303246; PMID:2363696
 A:Accession: S11127
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-5 <MIKI>
 A:Accession: S11128
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 'X', 2-5 <MIK2>
 C:Keywords: phosphoprotein

Query Match 27.3%; Score 9; DB 2; Length 5;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ISR 7
 |
 Db 3 VSK 5

RESULT 13

PT0525
 T-cell receptor beta chain V-D-J region (100-43) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0525
 R:Feeney, A.J.
 C. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0525
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <PEE>
 A:Experimental source: adult thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 27.3%; Score 9; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SR 7
 |
 Db 2 SR 3

RESULT 14

PT0577

T-cell receptor beta chain V-D-J region (141-180) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0577; PT0574
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0569; MUID:91277601; PMID:1711558
A:Accession: PT0577
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <PEE>
A:Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-180
A:Accession: PT0574
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <PE2>
A:Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-180
C:Keywords: T-cell receptor

Query Match 27.3% Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SR 7
|
Db 3 SR 4

RESULT 15
PT0565
T-cell receptor beta chain V-D-J region (141-180) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0565
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0569; MUID:91277601; PMID:1711558
A:Accession: PT0565
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <PEE>
A:Experimental source: day 19 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 27.3% Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SR 7
|
Db 3 SR 4

Search completed: October 4, 2003, 12:49:38
Job time : 20.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:27:32 ; Search time 10 Seconds
(without alignments)
32.913 Million cell updates/sec

Title: US-09-712-819C-6

Perfect score: 33

Sequence: 1 FTKISR ?

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 83

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	33.3	5	1 RE31_LITRU	P82072 Litoria rub
2	11	33.3	5	1 RE32_LITRU	P82073 Litoria rub
3	10	30.3	7	1 GFR1_MOUSE	P99025 mus musculus
4	9	27.3	5	1 UF01_MOUSE	P38639 mus musculus
5	9	27.3	6	1 UN06_CLOPA	P81351 clostridium
6	9	27.3	1	1 CCPI_ENTFA	P20104 enterococcus
7	9	27.3	7	1 CHOX_ALCSP	P16101 alcaligenes
8	9	27.3	7	1 CIA_ENTFA	P11932 enterococcus
9	9	27.3	7	1 UC21_MAIZE	P86630 zea mays
10	8	24.2	5	1 AL14_CARMA	P81817 carcinus ma
11	8	24.2	5	1 PSX_DAUCA	P58261 daucus caro
12	8	24.2	7	1 ALL2_CARMA	P81905 carcinus ma
13	8	24.2	7	1 ALL3_CARMA	P81306 carcinus ma
14	8	24.2	7	1 AL14_CARMA	P81807 carcinus ma
15	8	24.2	7	1 AL15_CARMA	P81308 carcinus ma
16	8	24.2	7	1 AL17_CDDPO	P82158 cydia pomon
17	8	24.2	7	1 CARP_MYTEO	P10420 mytilus edu
18	8	24.2	7	1 FAR5_HIRME	P42564 hirudo medi
19	7	21.2	3	1 LUXE_VIBFI	P24272 vibrio fisc
20	7	21.2	6	1 LCK1_LOCOM	P41431 locusta rig
21	7	21.2	6	1 VP19_HSV1K	P23210 herpes simp
22	6	18.2	4	1 ACHI_ACHFU	P35904 achatina fu
23	6	18.2	4	1 FAR3_HIRME	P42562 hirudo medi
24	6	18.2	4	1 FAR4_HIRME	P42563 hirudo medi
25	6	18.2	4	1 FFK4_ANTEL	P58735 antechpaura
26	6	18.2	4	1 FLRF_HIRME	P42561 hirudo medi
27	6	18.2	4	1 FLRN_ANTEL	P58707 antechpaura
28	6	18.2	4	1 FMRE_MACNI	P61162 macrocallis
29	6	18.2	4	1 FYRI_ANTEL	P58706 antechpaura
30	6	18.2	4	1 OCPI_COTN:	P58648 octopus min
31	6	18.2	5	1 E103_LITRU	P82099 Litoria rub
32	6	18.2	5	1 E104_LITRU	P82100 Litoria rub
33	6	18.2	5	1 FAR1_ANTTR	P41953 antiposth:

34	6	18.2	5	1 PAP2_PARMA	P81864 pardachirus
35	6	18.2	5	1 RE11_LITRU	P62470 Litoria rub
36	6	18.2	5	1 RE21_LITRU	P62371 Litoria rub
37	6	18.2	5	1 SUGA_ACHDO	P15991 acheta dome
38	6	18.2	5	1 TPIS_CANFA	P54714 canis famil
39	6	18.2	5	1 UC22_MAIZE	P80626 zea mays (m
40	6	18.2	6	1 ACPH_RABIT	P25154 oryctolagus
41	6	18.2	6	1 CIP1_MYTEO	P13736 mytilus edu
42	6	18.2	6	1 CIP2_MYTEO	P13737 mytilus edu
43	6	18.2	6	1 E101_LITRU	P82096 Litoria rub
44	6	18.2	6	1 FARP_MONEX	P41965 moniezia ex
45	6	18.2	7	1 E105_LITRU	P82101 Litoria rub

ALIGNMENTS

RESULT 1
RE31_LITRU
ID RE31_LITRU STANDARD; PRT: 5 AA.
AC P82072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
(1)
RN P82072;
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
'Litoria rubella'. The skin peptide profile as a probe for the study
of evolutionary trends of amphibians."
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MCD RES 5 5
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB1C30000C CRC64;
Query Match 33.3%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 FT 2
DB 4 FT 5

RESULT 2
RE32_LITRU
ID RE32_LITRU STANDARD; PRT: 5 AA.
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCB:TaxID=104895;
(1)
RN P82073;
RP SEQUENCE.
RC TISSUE=Skin secretion;

RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzy tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
 CC activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC Amphibian defense peptide.
 SW SEQUENCE 5 AA; 570 MW; 71A9C3C862A80000 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
 DB 4 FT 5

RESULT 3
 GFRP_MOUSE STANDARD; PRT; 7 AA.
 ID GFRP_MOUSE
 AC P99025;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE GTP cyclohydrolase 1 feedback regulatory protein (P19) (Fragment).
 GN GCHFR OR GFRP.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RA Sanchez J.-C., Rouge V., Fruiger S., Hughes G., Yan J.X.,
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
 RA Cowthorne M.;
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.
 CC -!- FUNCTION: MEDIATES TETRAHYDROOPTRIN INHIBITION OF GTP
 CC CYCLOHYDROLASE. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
 CC (BY SIMILARITY).
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC SWISS-2DPAGE; P99025; NCUSE.
 FT INIT MET 0
 FT NON TER 7
 SQ SEQUENCE 7 AA; 806 MW; 71B5B357273B4700 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 7;
 Best Local Similarity 75.0%; Pred. No. 1.3e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LKIS 6
 DB 3 LLIS 6

RESULT 4
 UF01_MOUSE STANDARD; PRT; 5 AA.
 ID UF01_MOUSE
 AC P38639;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Fibroblast;
 RX MEDLINE=95009507; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.S., He C., Solkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis";
 RL Electrophoresis 15:735-745(1994).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P1 OF THIS UNKNOWN
 CC PROTEIN IS: 6.6, ITS MW IS: 19 KDa.
 FT NON TER 5
 SQ SEQUENCE 5 AA; 717 MW; 7364087C4310C000 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ISR 7
 DB 2 IGR 4

RESULT 5
 UN06_CLOPA STANDARD; PRT; 6 AA.
 ID UN06_CLOPA
 AC P81351;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Unknown protein CP 6 from 2D-page (Fragment).
 CS Clostridium pasteurianum.
 CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 CC Clostridium.
 OX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=M5;
 RX MEDLINE=96291870; PubMed=962918;
 RA Flengsrud R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum W5";
 RL Electrophoresis 19:802-806(1998).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P1 OF THIS UNKNOWN
 CC PROTEIN IS: 5.0, ITS MW IS: 75.9 KDa.
 FT NON TER 6
 SQ SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TJKI 5
 DB 3 TAEI 6

RESULT 6
 CCF1_ENTFA STANDARD; PRT; 7 AA.
 ID CCF1_ENTFA
 AC P20104;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone cCF10.
 OS Enterococcus faecalis (Streptococcus faecalis).
 CC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=89008113; PubMed=3139658;
 RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
 RA Adsit J.C., Dunn Y.G.M., Suzuki A.;
 RT "Structure of cCF10, a peptide sex pheromone which induces
 RT conjugative transfer of the Streptococcus faecalis tetracycline
 RT resistance plasmid, pCF10";

RL J. Biol. Chem. 263:14574-14578(1988).
 CC -1- FUNCTION: CCF1C IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC HEMOLYSIN PLASMID PCF10.
 CC
 DR PIR: A30812; A30812.
 KW Pheromone. 7 AA; 790 MW; 7209202731E20740 CRC64;
 SQ SEQUENCE 7 AA; 790 MW; 7209202731E20740 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
 DB 3 TL 4

RESULT 7
 CHOX_ALUCSP STANDARD; PRT; 7 AA.
 ID CHOX_ALUCSP
 AC P16101;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last annotation update)
 DE Choline oxidase (EC 1.1.3.17) (Fragment).
 OS Alcaligenes sp.
 CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 CC Alcaligenaceae; Alcaligenes.
 CC NCB1_TaxID=512;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=8006769; PubMed=6997283;
 RA Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
 RT "Identification and properties of the prosthetic group of choline
 RT oxidase from Alcaligenes sp.";
 RL J. Biochem. 88:197-203(1983).
 CC -1- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
 DR PIR: A15398; A15398.
 KW Oxidoreductase.
 FT NON_TER
 SQ SEQUENCE 7 AA; 839 MW; 741931E457644AC0 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SR 7
 DB 6 SR 7

RESULT 8
 CIA_ENTFA STANDARD; PRT; 7 AA.
 ID CIA_ENTFA
 AC P11932;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
 CC Enterococcus faecalis (Streptococcus faecalis).
 CC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 CC NCB1_TaxID=1351;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=87005252; PubMed=3093276;
 RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
 RA White B.A., An F.Y., Clewell D.B., Suzuki A.;
 RA "Isolation and structure of the Streptococcus faecalis sex pheromone,
 RA CAM373.";
 RT CAM373.";
 RL FEBS Lett. 206:69-72(1986).
 CC -1- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
 CC HARBORING PAM373.
 CC
 CC -1- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR
 CC SPECIFICITY OF PHEROMONES TO PLASMIDS.

CC -1- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
 KW PIR: A25269; A25269.
 KW Pheromone. 7 AA; 734 MW; 75BD372059CC5D80 CRC64;
 SQ SEQUENCE 7 AA; 734 MW; 75BD372059CC5D80 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TL 3
 DB 3 TL 5

RESULT 9
 UC24_MAIZE STANDARD; PRT; 7 AA.
 ID UC24_MAIZE
 AC P80630;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 447)
 DE (Fragment).
 OS Zea mays (Maize).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 CC NCB1_TaxID=4577;
 RN [1]
 RP SEQUENCE
 RC T-SSUB=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Samerval C., Huet J.-C.,
 RA Pernolet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P1 OF THIS UNKNOWN
 CC PROTEIN IS: 6.0, ITS MW IS: 30.0 KDa.
 DR Maize-2DPAGE; P80630; COLEOPTILE.
 DR MaizeDB; 123956; -- 1
 FT NON_TER
 SQ SEQUENCE 7 AA; 665 MW; 6DC155B33DC1B5D0 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLX 4
 DB 2 TAK 4

RESULT 10
 ALI4_CARMA STANDARD; PRT; 5 AA.
 ID ALI4_CARMA
 AC P81817;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin A.
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 CC Eubrachyura; Portunioidea; Portunidae; Carcinus.
 CC NCB1_TaxID=6759;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the

RT allatostatin superfamily in the shore crab *Carcinus maenas*.
 RL Eur. J. Biochem. 250:727-734 (1997).
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD RES 5 5
 SQ SEQUENCE 5 AA; 586 MW; 672879D5AB30C00 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3
 DB 3 FGL 5

RESULT 11
 ID PSK DAUCA STANDARD; PRT; 5 AA.
 AC P81807;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)].
 OS Daucus carota (Carrot).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; campanulids; Apiales; Apiaceae; Daucus.
 NCBI_TaxID=4039;
 RN [1]
 RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.
 RC STRAIN=cv. US-Harumakigcsun;
 RX MEDLINE=20212743; PubMed=10730785;
 RA Harai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T., Kanada H., Sakagami Y.;
 RT "A secreted peptide growth factor, phytosulfokine, acting as a stimulatory factor of carrot somatic embryo formation.";
 RL Plant Cell Physiol. 41:127-132 (2000).
 CC -1- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC ENBRYS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.
 CC Growth factor; Sulfation.
 KW PEPTIDE 1 4 PHYTOSULFOKINE-BETA.
 FT MOD RES 1 4
 FT MOD RES 3 3 SULFATION.
 SQ SEQUENCE 5 AA; 487 MW; 76C1B5045300000 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTL 2
 DB 3 FGL 4

RESULT 12
 ID ALL2 CARMA STANDARD; PRT; 7 AA.
 AC P81805;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 2.
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab *Carcinus maenas*.";
 RL Eur. J. Biochem. 250:727-734 (1997).
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD RES 7 7
 FT MOD RES 7 7 AMIDATION (POTENTIAL).
 SQ SEQUENCE 7 AA; 770 MW; 672879DCB5DD87C CRC64;

Query Match 24.2%; Score 8; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3
 DB 5 FGL 7

RESULT 13
 ID ALL3 CARMA STANDARD; PRT; 7 AA.
 AC P81806;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 3.
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab *Carcinus maenas*.";
 RL Eur. J. Biochem. 250:727-734 (1997).
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Multigene family.
 SQ SEQUENCE 7 AA; 756 MW; 672879DCB47689C CRC64;

Query Match 24.2%; Score 8; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3
 DB 5 FGL 7

RESULT 14
 ID ALL4 CARMA STANDARD; PRT; 7 AA.
 AC P81807;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 4.
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

CC Eubrachyura; Portunioidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [-]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab *Carcinus maenas*."
 RL Eur. J. Biochem. 250:727-734 (1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 SQ SEQUENCE 7 AA; 782 MW; 672879CDCB476AC0 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3
 | |
 Db 5 FGL 7

RESULT 15
 ALL5 CARMA
 ID -ALL5 CARMA STANDARD; FRT; 7 AA.
 AC P81A08;
 DT 30-MAY-2000 (Rel. 33, Created)
 DT 30-MAY-2000 (Rel. 33, Last sequence update);
 DT 30-MAY-2000 (Rel. 33, Last annotation update)
 DE Carcinustatin 5.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [-]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab *Carcinus maenas*."
 RL Eur. J. Biochem. 250:727-734 (1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD RES 7
 FT MOD RES 7
 SQ SEQUENCE 7 AA; 791 MW; 672879CDCB476420 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3
 | |
 Db 5 FGL 7

Search completed: October 4, 2003, 12:46:01
 Job time : 10 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:40:19 ; Search time 48 seconds
(without alignments)
37.633 Million cols: updates/soc

Title: US-09-712-819C-6

Perfect score: 33

Sequence: 1 FTLKISR 7

Scoring table: B:G:SUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 256052604 residues

Total number of hits satisfying chosen parameters: 67

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:

- 1: sp_archea:
- 2: sp_bacteria:
- 3: sp_fungi:
- 4: sp_human:
- 5: sp_invertebrate:
- 6: sp_mammal:
- 7: sp_mic:
- 8: sp_organelle:
- 9: sp_plant:
- 10: sp_plant:
- 11: sp_rodent:
- 12: sp_virus:
- 13: sp_vertebrate:
- 14: sp_unclassified:
- 15: sp_virus:
- 16: sp_bacteriopl:
- 17: sp_archea:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	13	39.4	6	10	P82181
2	13	39.4	6	10	P82182
3	11	33.3	7	8	Q95945
4	10	30.3	6	10	P82541
5	9	27.3	4	11	Q08433
6	9	27.3	7	2	Q07354
7	9	27.3	7	2	Q8GL12
8	9	27.3	7	2	Q8GL12
9	9	27.3	7	2	Q8GL12
10	9	27.3	7	4	Q15637
11	9	27.3	7	10	P92213
12	9	27.3	7	11	Q8K3H6
13	9	27.3	7	11	Q63480
14	5	27.3	7	11	Q55184
15	9	27.3	7	15	Q8UE81
16	8	24.2	7	2	P70804

Q47029 enterobacte
Q9YVE3 human adeno
Q9YVQ9 human adeno
Q9YVQ9 human adeno
P83073 bacillus ce
P72081 nocardia la
Q9YVQ9 homo sapien
Q66205 transmissib
Q9YVQ9 transmissib
P43308 gallus gall
Q53556 actinobacill
Q54248 streptomyce
Q8KMS9 enterobacte
Q34228 sphingomona
Q15903 homo sapien
Q28742 oryctolagus
P22214 amblyopyrum
P92393 hordeum vul
P92433 lophopyrum
P92427 peridictyon
P92430 aegilops ta
P92221 bromus iner
Q98966 spiracia ol
P92425 pseudoroegn
P92381 hordeum bra
P92387 horcardia p
P92200 agropyron c
P92440 thiropyrum
P92218 australopyr

ALIGNMENTS

RESULT 1

P82181 ID P82181 PRELIMINARY; PRT; 6 AA.

AC P82181; 01-JUN-2000 (TrEMBLrel. 14, Created)

DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Chloroplast 50S ribosomal protein L10 beta (Fragment).

OS Spinacia oleracea (Spinach).

CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

CC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.

CX NCBI_TaxID=3562;

RN (1)

RP SEQUENCE.

RC STRAIN=cv. ALMARO; TISSUE=Leaf;

RX MEDLINE=20435798; PubMed=10874046;

RA Yamaguchi K., Subramanian A.R.;

RT "The plastid ribosomal proteins. Identification of all the proteins in

RT J. Biol. Chem. 275:28466-28482(2000).

CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.

CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.

CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.

CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.

CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.

DR Interpro: IPR001790; Ribosomal_L10.

DR Interpro: IPR002363; Ribosomal_L10eub.

DR Pfam: PF00466; Ribosomal_L10; PARTIAL.

DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.

KW Ribosomal protein; Chloroplast; rRNA-binding.

FT NON TER 6

SQ SEQUENCE 6 AA; 675 MW; 63218415B05DB00C CRC64;

Query Match: 39.4%; Score 13; DB 10; Length 6;

Best Local Similarity 100.0%; Pred. NC. 8.3e-05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISR 7

RX MEDLINE=91282759; PubMed=1645486;
RA Sato H., Aono S., Kashiwamata S., Koizumi O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
DR EMBL; S38636; AAB19259.1; -;
KW Transferase.
FT NON TER 1 1
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 27.3%; Score 9; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.3e+5;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LK 4
DB 3 LK 4

RESULT 6
O07354 PRELIMINARY; PRT; 7 AA.
AC O07354;
DT 01-JUL-1997 (TrEMBLrel. 04, Created);
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update);
DT 01-DEC-2002 (TrEMBLrel. 19, Last annotation update);
DE Nifk (Fragment).
GN NIFK.
OS Synechococcus sp. (strain PCC 8801 / RP-1) (Cyanothecae PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
OX NCBI_TaxID=41431;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RP-1;
RX MEDLINE=99231361; PubMed=10217509;
RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
RT "Organization and expression of nitrogen-fixation genes in the aerobic
nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
RP-1.";
RL Microbiology 145:743-753(1999).
DR EMBL; AF003700; AAC35193.1; -;
FT NON TER 1 1
SQ SEQUENCE 7 AA; 849 MW; 7412C72AA9D5E030 CRC64;

Query Match 27.3%; Score 9; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FT; 3
DB 3 FOL 5

RESULT 7
O07312 PRELIMINARY; PRT; 7 AA.
AC O07312;
DT 01-MAR-2003 (TrEMBLrel. 23, Created);
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-9.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N40;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
prophages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142106; AAN17857.1; -;
KW Plasmid.
FT NON TER 1 1
SQ SEQUENCE 7 AA; 928 MW; 6337233050417350 CRC64;

DR EMBL; AY142100; AAN17911.1; -;
KW Plasmid.
FT NON TER 1 1
SQ SEQUENCE 7 AA; 849 MW; 6337244330569ED0 CRC64;

Query Match 27.3%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LK 4
DB 6 LK 7

RESULT 8
O8GL04 PRELIMINARY; PRT; 7 AA.
AC O8GL04;
DT 01-MAR-2003 (TrEMBLrel. 23, Created);
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-5.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=93-0107;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
prophages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142103; AAN17848.1; -;
KW Plasmid.
FT NON TER 1 1
SQ SEQUENCE 7 AA; 914 MW; 6337244330504310 CRC64;

Query Match 27.3%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LK 4
DB 6 LK 7

RESULT 9
O8GL00 PRELIMINARY; PRT; 7 AA.
AC O8GL00;
DT 01-MAR-2003 (TrEMBLrel. 23, Created);
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-13.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CA15;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
prophages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142106; AAN17857.1; -;
KW Plasmid.
FT NON TER 1 1
SQ SEQUENCE 7 AA; 928 MW; 6337233050417350 CRC64;

Query Match 27.3%; Score 9; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LK 4
 ||
 Db 6 LK 7

RESULT 10
 Q15897 Q15897 PRELIMINARY; PRT; 7 AA.
 ID Q15897;
 AC Q15897;
 DT 01-NOV-1996 (TREMBlrel. 01, Created);
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update);
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update);
 DE (Clone XP6A11A) (Fragment);
 OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
 ON NCBI_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Lee C.-C., Yazdani A., Kennert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
 RA Caskey C.T.H.;
 RT "Isolation of chromosome-specific genes by reciprocal probing of
 RT arrayed cDNAs and cosmid libraries";
 RL Hum. Mol. Genet. 4:0-5(1995).
 DR EMBL; L32077; AAA73887.1; --
 FT NON TER 1
 FT NON TER 7
 SQ SEQUENCE 7 AA; 814 MW; 672B1DD3372546B0 CRC64;

Query Match 27.3%; Score 9; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LK 4
 ||
 Db 3 LK 4

RESULT 11
 P93233 P93233 PRELIMINARY; PRT; 7 AA.
 ID P93233;
 AC P93233;
 DT 01-MAY-1997 (TREMBlrel. 03, Created);
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update);
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update);
 DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14);
 DE (Fragment);
 GN JE-ACSIB;
 OS Lycopersicon esculentum (Tomato);
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Lamiales; Solanales; Solanaceae; Solanum;
 ON NCBI_TaxID=4081;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97351561; PubMed=9207843;
 RA Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;
 RA "Differential induction of seven 1-aminocyclopropane-1-carboxylate
 RT synthase genes by elicitor in suspension cultures of tomato
 RT (Lycopersicon esculentum).";
 RL Plant Mol. Biol. 34:275-286(1997).
 DR EMBL; U75692; AAC49682.1; --
 FT NON TER 1
 FT NON TER 7
 SQ SEQUENCE 7 AA; 828 MW; 7B412C7377415D0 CRC64;

Query Match 27.3%; Score 9; DB 10; Length 7;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SR 7
 ||
 Db 1 SR 2

RESULT 12
 Q8K3H6 Q8K3H6 PRELIMINARY; PRT; 7 AA.
 ID Q8K3H6;
 AC Q8K3H6;
 DT 01-OCT-2002 (TREMBlrel. 22, Created);
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update);
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update);
 DE Collagenase-3 (Fragment);
 GN MMP13;
 OS Rattus norvegicus (Rat);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
 ON NCBI_TaxID=10116;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Prietto S.M., Lyons J.G.;
 RA "Insertion 1 of Rattus norvegicus MMP13";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AF101357; AAM51172.1; --
 FT NON TER 1
 FT NON TER 7
 SQ SEQUENCE 7 AA; 907 MW; 63373B51E31DD9A0 CRC64;

Query Match 27.3%; Score 9; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LK 4
 ||
 Db 6 LK 7

RESULT 13
 Q63480 Q63480 PRELIMINARY; PRT; 7 AA.
 ID Q63480;
 AC Q63480;
 DT 01-NOV-1996 (TREMBlrel. 01, Created);
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update);
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update);
 DE TR4-NS orphan receptor (Fragment);
 GN TR4;
 OS Rattus norvegicus (Rat);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
 ON NCBI_TaxID=10116;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96198747; PubMed=8612486;
 RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
 RA Betera-Wadleigh S.D.;
 RT "Splice variants of rat TR4 orphan receptor: differential expression
 RT of novel sequences in the 5'-untranslated region and C-termina
 RL domain.";
 RL Endocrinology 137:1562-1571(1996).
 DR EMBL; U59125; AAB02827.1; --
 KW Receptor.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 7 AA; 758 MW; 672AA878640C5350 CRC64;

Query Match 27.3%; Score 9; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KI 5

Db 2 KI 2
Query Match 27.3%; Score 9; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 TL 3
Db 4 TL 5

Search completed: October 4, 2003, 12:48:32
Run time: 48 secs

RESULT 14
O55184
ID O55184 PRELIMINARY; PRT; 7 AA.
AC O55184
DT 01-JUN-1998 (TREMBlrel: 26, Created)
DT 01-JUN-1998 (TREMBlrel: 26, Last sequence update)
DT 01-DEC-2001 (TREMBlrel: 19, Last annotation update)
DE Orphan receptor TR4-NS (Fragment).
GN GN
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
[1]
RN RATTUS NORVEGICUS (RAT).
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=96189747; PubMed=8612486;
RA Yoshikawa T., Makino S., Gao X.M., King S.C., Chuang D.M.,
RA Detera-Wadleigh S.D.;
RI "Splice variants of rat TR4 orphan receptor: differential expression
of novel sequences in the 5'-untranslated region and C-terminal
domain."
RT Endocrinology 137:1562-1571(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=96299786; PubMed=8661150;
RA Yoshikawa T., DuPont B.R., Leach R.J., Detera-Wadleigh S.D.;
RI "New variants of the human and rat nuclear hormone receptor, TR4:
expression and chromosomal localization of the human gene";
RL Genomics 35:361-366(1996).
DR EMBL; U59454; AAB91433.1; -.
KW Receptor.
FT NON_TER
SQ SEQUENCE 7 AA; 563 MW; 6DDAA8787EB535C CRC64;

Query Match 27.3%; Score 9; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 KI 5
Db 1 KI 2

RESULT 15
O8JEB1
ID O8JEB1 PRELIMINARY; PRT; 7 AA.
AC O8JEB1
DT 01-OCT-2002 (TREMBlrel: 22, Created)
DT 01-OCT-2002 (TREMBlrel: 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel: 22, Last annotation update)
DE Truncated pol protein (fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
CX NCBI_TaxID=11676;
[1]
RN HUMAN IMMUNODEFICIENCY VIRUS 1.
RP SEQUENCE FROM N.A.
RC STRAIN=4874;
RX MEDLINE=22056123; PubMed=12060770;
RA Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
RA Hoffmann D., Korn K., Selbig J.;
RI "Diversity and complexity of HIV-1 drug resistance: A bioinformatics
approach to predicting phenotype from genotype."
RL Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
DR EMBL; AF347267; AAK32344.1; -.
FT NON_TER
SQ SEQUENCE 7 AA; 925 MW; 76C37731A046C70C CRC64;

PS Disclosure; Page 6; 105pp; English.

XX Sequences AAY40727-Y40748 are functionally equivalent derivatives of the

CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a

CC beta strand peptide which forms part of a beta sheet. Peptides

CC (AAY40601-Y40609) together form a single-chain scaffold protein which

CC contains at least 1 disulfide bond, contains less than 10% alpha helix

CC and contains at least 6 beta-strands. The scaffold protein is constructed

CC of beta strands S1-S6, and may also include beta strands A1-A3, or any

CC functionally equivalent derivative of these sequences. The beta strands

CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to

CC the next by hydrogen bonds, which generate a beta sandwich architecture.

CC If the additional beta strands A1-A3 are included in the structure the

CC scaffold is constructed of two beta sheets, with the structures

CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each

CC other via amino acid loops, where at least one of the loops binds to a

CC receptor or antigen. The scaffold protein is used to stabilize antigens

CC to bind two separate molecules. For example, one surface of the scaffold

CC may be bound to a protein which binds to a tumour antigen. This will

CC target the complex to tumour cells. Another surface may be bound to a

CC cytotoxic molecule or an autoimmune antibody which may then kill the

CC tumour cells. Therefore the scaffold protein may be used to target

CC chemotherapeutic agents to specific cells. It may also be used to

CC stabilize individual peptides in a peptide library and may be used in

CC diagnostic techniques, and to stabilize antigens used as vaccines.

XX

SEQ Sequence 7 AA;

Query Match 59.7%; Score 23; DB 20; Length 7;

Best Local Similarity 83.3%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKIS 6

DB 2 FTLNIS 7

RESULT 2

AAB30074

ID AAB30074 standard; Peptide; 7 AA.

AC AAB30074;

XX

DT 09-FEB-2001 (first entry)

XX

DE Scaffold protein SCA S4 peptide SEQ ID NO: 135.

XX

XX Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;

XX SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;

XX diabetic retinopathy; atherosclerosis.

XX

OS Synthetic.

XX

XX WC2000060070-A1.

XX

PD 12-OCT-2000.

XX

XX 01-APR-1999; 99WO-EP2283.

XX

PR 01-APR-1999; 99WO-EP2283.

XX

PA (INNO-) INNOGENETICS NV.

XX

P- Desmet J, Hufton S, Hoogenboom H, Sablon E;

XX

XX WPI; 2003-665002/64.

XX

PT Scaffold composed of single-chain polypeptide having beta sandwich

PT architecture carrying new and randomized peptide sequences useful as

PT supporting framework and carrying antigen- or receptor binding

PT fragments

XX

PS Disclosure; Page 15; 68pp; English.

XX The present invention is concerned with producing scaffold proteins

CC based upon the human CTLA-4 SCA domain. These scaffold proteins can be

CC used as a scaffold to bind antigen- or receptor-binding fragments. These

CC can be used in the treatment of diseases such as cancer,

CC atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and

CC diabetic retinopathy. Sequences AAB29330-B29339 were used in the

CC production of the proteins of the invention.

XX

SEQ Sequence 7 AA;

Query Match 69.7%; Score 23; DB 21; Length 7;

Best Local Similarity 83.3%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKIS 6

DB 2 FTLNIS 7

RESULT 3

AAY40738

ID AAY40738 standard; peptide; 7 AA.

XX

AC AAY40738;

XX

DT 01-DEC-1999 (first entry)

XX

DE S4 derivative #12, beta strand of scaffold protein structure.

XX

XX Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;

XX tumour; chemotherapeutic agent.

XX

OS Synthetic.

XX

PN EP947592-A1.

XX

PD 06-OCT-1999.

XX

XX 31-MAR-1998; 98EP-0870065.

XX

PF 31-MAR-1998; 98EP-0870065.

XX

PR 31-MAR-1998; 98EP-0870065.

XX

PA (INNO-) INNOGENETICS NV.

XX

XX Desmet J, Hufton S, Hoogenboom H, Sablon E;

XX

XX WPI; 1999-542959/46.

XX

PT New scaffold protein, useful for stabilizing antigens used as vaccines

PT

XX

XX Disclosure; Page 6; 105pp; English.

XX

CC Sequences AAY40727-Y40748 are functionally equivalent derivatives of the

CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a

CC beta strand peptide which forms part of a beta sheet. Peptides

CC (AAY40601-Y40609) together form a single-chain scaffold protein which

CC contains at least 1 disulfide bond, contains less than 10% alpha helix

CC and contains at least 6 beta-strands. The scaffold protein is constructed

CC of beta strands S1-S6, and may also include beta strands A1-A3, or any

CC functionally equivalent derivative of these sequences. The beta strands

CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to

CC the next by hydrogen bonds, which generate a beta sandwich architecture.

CC If the additional beta strands A1-A3 are included in the structure the

CC scaffold is constructed of two beta sheets, with the structures

CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each

CC other via amino acid loops, where at least one of the loops binds to a

CC receptor or antigen. The scaffold protein is used to stabilize antigens

CC to bind two separate molecules. For example, one surface of the scaffold

CC may be bound to a protein which binds to a tumour antigen. This will

CC target the complex to tumour cells. Another surface may be bound to a
CC cytotoxic molecule or an autoimmune antibody which may then kill the
CC tumour cells. Therefore the scaffold protein may be used to target
CC chemotherapeutic agents to specific cells. It may also be used to
CC stabilize individual peptides in a peptide library and may be used in
CC diagnostic techniques, and to stabilize antigens used as vaccines.

XX Sequence 7 AA;

Query Match 66.7%; Score 22; DB 20; Length 7;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKIS 6
DB 2 FLLTIS 7

RESULT 4
AAB30076
ID AAB30076 standard; Peptide; 7 AA.

AC AAB30076;

DF 09-FEB-2001 (first entry)

DE Scaffold protein SCA S4 peptide SEQ ID NO: 137.

Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;
diabetic retinopathy; atherosclerosis.

OS Synthetic.

XX WO20060070-A1.

XX 12-OCT-2000.

PF 01-APR-1999; 99WO-EP02283.

PR 01-APR-1999; 99WO-EP02283.

PA (INNO-) INNOGENETICS NV.

PI Desmet J, Hufton S, Hoogenboom H, Sablon E;

DR WPI; 2000-665002/64.

Scaffold composed of single-chain polypeptide having beta sandwich
architecture carrying new and randomized peptide sequences useful as
supporting framework and carrying antigen- or receptor binding
fragments.

PS Disclosure; Page 15; 68pp; English.

The present invention is concerned with producing scaffold proteins
based upon the human CTLA-4 SCA domain. These scaffold proteins can be
used as a scaffold to bind antigen- or receptor-binding fragments. These
can be used in the treatment of diseases such as cancer,
atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and
diabetic retinopathy. Sequences AAB329930-B29939 were used in the
production of the proteins of the invention.

XX Sequence 7 AA;

Query Match 66.7%; Score 22; DB 21; Length 7;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKIS 6
DB 2 FLLTIS 7

RESULT 5

AAY42013
ID AAY42013 standard; Peptide; 7 AA.

XX AAY42013;

DF 09-DEC-1999 (first entry)

DE Rheumatoid arthritis diagnostic protein isoform peptide #164.

Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;
rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;
rheumatoid arthritis diagnostic protein isoform; screening;
expression reference protein isoform; prognosis.

OS Homo sapiens.

XX WO9947925-A2.

XX 23-SEP-1999.

PF 15-MAR-1999; 99WO-GB00763.

PR 13-MAR-1998; 98GB-C005477.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Parekh RB, Patel TP, Townsend RR;

XX WPI; 1999-571871/48.

DR Diagnosis of human rheumatoid arthritis by two-dimensional
electrophoresis.

PS Disclosure; Page 21; 157pp; English.

A method has been developed for the diagnosis of human rheumatoid
arthritis (RA) using two-dimensional electrophoresis to generate a
two-dimensional array of features. The method can be used for screening,
diagnosis and prognosis of RA in a subject or for monitoring the effect
of an anti-RA drug or therapy administered to a subject. The method
comprises: (a) analysing a sample of serum or plasma and optionally
synovial fluid by two-dimensional electrophoresis, to generate a two-
dimensional array of features; (b) identifying at least one chosen
feature whose relative abundance correlates with the presence or absence
of RA; and (c) comparing the abundance of each chosen feature in the
sample with the abundance of that chosen feature in serum or plasma from
one or more persons without RA, where the relative abundance of the
chosen feature or features in the sample indicates the presence or
absence of RA in the subject. The method can also be used in clinical
studies for testing drugs for therapy of RA, for purification of RA-
diagnostic protein isoforms (RPIs), and for production of antibodies to
RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify
compounds that promote or inhibit their activity, which are then used as
RA drugs. Nucleic acid encoding RADFs can be used in gene therapy
protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to
AAY42103 represent expression reference protein isoform peptides and
AAZ25066 to AAZ25068 represent degenerate probes for RPIs, which are all
used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 63.6%; Score 21; DB 20; Length 7;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKISR 7
DB 2 TLMISR 7

RESULT 6

AA81848
ID AAR81848 standard; peptide; 7 AA.
XX
AC AAR81848;
XX
DT 16-MAY-1996 (first entry);
XX
XX Human afamin tryptic fragment FX20.
DE
XX Human; afamin; serum protein family; albumin; alpha-fetoprotein; plasma;
KW vitamin D binding protein; homology; post-translational processing;
KW chromatography; primer; PCR; amplification; probe; rheumatoid arthritis;
KW ischaemia-reperfusion injury; ARDS; cardiopulmonary bypass; sepsis;
KW toxic plasma substance; inflammation.
XX
OS Homo sapiens.
XX
XX WO9527059-A1.
PN
XX
PD 12-OCT-1995.
XX
XX 31-MAR-1995; 95WO-US04075.
PF
XX 31-MAR-1994; 94US-0222619.
PR
XX (AMGE-) AMGEN INC.
PA (UVRQ) UNIV ROCKEFELLER.
XX
XX Lichenstein HS, Lyons DE, Wright SD, Wurfel XM;
PI WPI; 1995-358634/46.
DR
XX Human afamin or a variant and polynucleotide(s) encoding it - a
PT human serum protein with activities in common with other members of
PT this family.
XX
FS Example 3; Page 45; 97pp; English.
XX
XX Peptides AAR81847-54 are tryptic peptide fragments from human afamin
CC (AAR81845) novel member of the human serum protein family. The
CC fragments were used to design primers and probes (AATCC786-98) for the
CC cloning of the afamin gene (AATC0785) from human liver cDNA. Afamin is
CC thought to have similar properties to human albumin, alpha-fetoprotein
CC and vitamin D binding protein due to homology with these proteins. The
CC gene encodes a mature protein of 66376 daltons without post-translational
CC processing (ca. 97000 daltons with post-translational processing). The
CC protein was isolated from human plasma by a conventional chromatographic
CC methods. The protein can be used to ameliorate ischaemia-reperfusion
CC injury, rheumatoid arthritis, ARDS, cardiopulmonary bypass, sepsis, toxic
CC plasma substances released after inflammation, etc.
XX
SQ Sequence 7 AA;
Query Match 50.61; Score 20; FR 15; Length 7;
Best Local Similarity 57.14; Pred. No. 9.3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 FTLKISR 7
|||
Db 1 FTPEYSR 7
|||
RESULT 7
AAAY41889
ID AAY41889 standard; Peptide; 7 AA.
XX
XX AAY41889;
AC
XX
XX 09-DEC-1999 (first entry);
DT
XX Rheumatoid arthritis diagnostic protein isoform peptide #40.
DE
XX Human; rheumatoid arthritis; RA; diagnosis; RP1; RAD7; detection;
KW

KW rheumatoid arthritis diagnostic feature; RP1; synovial fluid;
KW rheumatoid arthritis diagnostic protein isoform; screening;
KW expression reference protein isoform; prognosis.
XX
XX Homo sapiens.
OS
XX WO9947925-A2.
PN
XX 23-SEP-1999.
PD
XX 15-MAR-1999; 99WO-GB00763.
PF
XX 13-MAR-1998; 98GB-0005477.
PR
XX (OXFC-) OXFORD GLYCOSCIENCES UK LTD.
PA
XX Parekh RB, Patel TP, Townsend RR;
PI WPI; 1999-571871/46.
DR
XX Diagnosis of human rheumatoid arthritis by two-dimensional
PT electrophoresis -
PT
XX Disclosure, Page 18; 157pp; English.
XX
XX A method has been developed for the diagnosis of human rheumatoid
CC arthritis (RA) using two-dimensional electrophoresis to generate a
CC two-dimensional array of features. The method can be used for screening,
CC diagnosis and prognosis of RA in a subject or for monitoring the effect
CC of an anti-RA drug or therapy administered to a subject. The method
CC comprises: (a) analysing a sample of serum or plasma and optionally
CC synovial fluid by two-dimensional electrophoresis, to generate a two-
CC dimensional array of features; (b) identifying at least one chosen
CC feature whose relative abundance correlates with the presence or absence
CC of RA; and (c) comparing the abundance of each chosen feature in the
CC sample with the abundance of that chosen feature in serum or plasma from
CC one or more persons without RA, where the relative abundance of the
CC chosen feature or features in the sample indicates the presence or
CC absence of RA in the subject. The method can also be used in clinical
CC studies for testing drugs for therapy of RA, for purification of RA-
CC diagnostic protein isoforms (RPIs), and for production of antibodies to
CC RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify
CC compounds that promote or inhibit their activity, which are then used as
CC RA drugs. Nucleic acid encoding RADFs can be used in gene therapy
CC protocols. AAY41844 to AAY42100 represent RPI peptides. AAY42101 to
CC AAY42103 represent expression reference protein isoform peptides and
CC AAY25066 to AAY25068 represent degenerate probes for RPIs, which are all
CC used in the exemplification of the present invention.
XX
SQ Sequence 7 AA;
Query Match 50.61; Score 20; DB 20; Length 7;
Best Local Similarity 42.94; Pred. No. 9.3e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 FTLKISR 7
|||
Db 1 YTFELSR 7
|||
RESULT 8
ABE55570
ID ABE55570 standard; Peptide; 7 AA.
XX
XX ABE55570;
AC
XX
XX 15-FEB-2002 (first entry)
DT
XX Vascular dementia-associated protein isoform (VPI) 70.
DE
XX Vascular Dementia; VD; VD-associated protein isoform; VP1; screening;
KW diagnosis; prognosis; gene therapy.
XX

S	Homo sapiens.
N	WO200169261-A2.
X	
D	20-SEP-2001.
X	
F	14-MAR-2001; 2001WO-GS01106.
X	
R	15-MAR-2000; 2000GB-C006285.
R	24-NOV-2000; 2000GB-C028734.
R	28-NOV-2000; 2000US-C724391.
R	
A	(OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX	
P	Herath HMAC, Parekh RP, Rohlf C;
XX	
PI	WPI; 2001-557637/62.
XX	
T	Screening, diagnosis or prognosis of vascular dementia (VD), useful for
T	determining stage of VD and monitoring the effect of VD therapy; for
T	comprises analysing body fluid by 2-dimensional electrophoresis for
T	features correlated with VD -
X	
X	Claim 6; Page 31; 151pp; English.
S	
S	The invention relates to screening, diagnosis or prognosis of Vascular
X	Dementia (VD) in a subject comprising analysing body fluid from the
C	subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
C	features containing at least one chosen feature whose relative abundance
C	correlates with the presence, absence, stage or severity of VD or
C	predicts the onset or course of VD, especially detecting in a sample of
C	cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
C	protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
C	specification. Detecting VD-associated features and VPI is useful for the
C	screening, diagnosis or prognosis of VD, for determining the stage or
C	severity of VD, for identifying a subject at risk of VD or for
C	monitoring the effect of therapy administered to a subject having VD.
C	Nucleic acids encoding a VPI or inhibiting the function of a VPI are
C	useful for the treatment of VD and for gene therapy.
XX	
XQ	Sequence 7 AA;
	Query Match 60.6%; Score 20; DB 22; Length 7;
	Best Local Similarity 42.9%; Pred.No. 9.3e+05;
	Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0
DY	1 FTLKISR 7
Db	1 YTFELSR 7
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ID	ABB55981
CC	ABBS5981 standard; Peptide; 7 AA.
XX	
CC	ABBS5981;
XX	
CC	
DP	15-FEB-2002 (first entry)
XX	
DE	Vascular dementia-associated protein isoform (VPI) 181.
XX	
KX	Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
XX	diagnosis; prognosis; gene therapy.
XX	
DS	Homo sapiens.
XX	
EN	WO200169261-A2.
XX	
EN	
DD	20-SEP-2001.
XX	
PP	14-MAR-2001; 2001WO-GS01106.
XX	
PR	15-MAR-2000; 2000GB-C006285.

```

PR 24-NOV-2000; 2000GB-0028734.
FR 28-NOV-2000; 2000US-0724391.
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX Herath HMAC, Parekh RB, Rohlf C;
XX WPI; 2001-557937/62.
XX
XX Screening, diagnosis or prognosis of vascular dementia (VD); useful for
XX determining stage of VD and monitoring the effect of VD therapy.
XX PT Comprises analysing body fluid by 2-dimensional electrophoresis for
XX PT features correlated with VD -
XX
XX Claim 6; Page 33; 151pp; English.
XX
XX The invention relates to screening, diagnosis or prognosis of Vascular
XX Dementia (VD) in a subject comprising analysing body fluid from the
XX subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
XX CC features containing at least one chosen feature whose relative abundance
XX CC correlates with the presence, absence, stage or severity of VD or
XX CC predicts the onset or course of VD, especially detecting in a sample of
XX CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
XX CC protein isoforms (VPIs) (AB55801-AB56295) as fully defined in the
XX CC specification. Detecting VD-associated features and VPI is useful for the
XX CC screening, diagnosis or prognosis of VD, for determining the stage or
XX CC severity of VD, for identifying a subject at risk of VD or for
XX CC monitoring the effect of therapy administered to a subject having VD.
XX CC Nucleic acids encoding a VPI or inhibiting the function of a VPI are
XX CC useful for the treatment of VD and for gene therapy.
XX
XX Sequence 7 AA;
SQ
Query Match 62.6%; Score 20; DB 22; Length 7;
Best Local Similarity- 42.9%; Pred.No. 9.3e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0
QY : FTLKISR 7
Db 1 YTFELSR 7
: : : : :
: : : : :
RESULT 10
AB556283
ID ID AB556283 standard; Peptide; 7 AA.
AC AC AB556283;
XX
XX DT 15-FEB-2002 (first entry)
XX
XX DE Vascular dementia-associated protein isoform (VPI); 483.
XX
XX KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
XX KM diagnosis; prognosis; gene therapy.
XX
XX OS Homo sapiens.
XX
XX PN WO200169261-A2.
XX
XX PD 20-SEP-2001.
XX
XX PF 14-MAR-2001; 2001WO-GB01106.
XX
XX PR 15-MAR-2000; 2000GB-0006285.
XX PR 24-NOV-2000; 2000GB-0028734.
XX PR 28-NOV-2000; 2000US-0724391.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX Herath HMAC, Parekh RB, Rohlf C;
XX WPI; 2001-557937/62.
XX
XX
XX
XX

```

PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for
 PT determining stage of VD and monitoring the effect of VD therapy.
 PT comprises analysing body fluid by 2-dimensional electrophoresis for
 PT features correlated with VD.
 XX Claim 6; Page 40; 15pp; English.
 XX
 CC The invention relates to screening, diagnosis or prognosis of Vascular
 CC Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance
 CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
 CC protein isoforms (VPIs) (AB35801-AB35895) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for
 CC monitoring the effect of therapy administered to a subject having VD.
 CC Nucleic acids encoding a VPI or inhibiting the function of a VPI are
 CC useful for the treatment of VD and for gene therapy.
 XX
 SQ Sequence 7 AA;

Query Match 60.6%; Score 20; DB 22; Length 7;
 Best Local Similarity 42.9%; Pred. No. 9.3e-05;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy i FTUKISR 7
 Db : : : : :
 1 YTFELSR 7

RESULT 11
 ABB52190
 ID ABB52190 standard; Peptide; 7 AA.
 XX
 AC ABB52190;
 XX
 DT 08-FEB-2002 (first entry)
 XX
 DE Human API-146 tryptic digest peptide #1.
 XX
 KW Human; neuroprotective; nontopic; gene therapy; vaccine;
 KW Alzheimer's Disease; Alzheimer's Disease-Associated Feature; AF;
 KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
 KW Expression Reference Protein Isoform; ERPI; proteolysis.
 XX
 OS Homo sapiens.
 XX
 PN WO200175454-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 03-APR-2001; 2001WO-US10908.
 XX
 PR 03-APR-2000; 2000US-194504P.
 PR 28-NOV-2000; 2000US-253647P.
 XX
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA (PFIZ) PFIZER INC.

Durham KL, Friedman DL, Horath HMAc, Kimmel LH, Parekh RB;
 Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;
 Townsend RR, White F, Williams SA;
 WPI; 2001-639384/73.
 Screening for Alzheimer's disease in a mammal, by making
 two-dimensional array of a feature whose relative abundance correlates
 with disease, and comparing with abundance of the feature in samples of
 healthy persons

Example; Page 34; 162pp; English.
 The invention relates to methods for the screening, diagnosis and
 prognosis of Alzheimer's disease. The methods involve the detection
 of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
 Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
 serum or plasma. The abundance of the AFs and APIs is then
 normalised to an Expression Reference Protein Isoform (ERPI) in
 order to determine whether a patient is suffering from, or has

PS Example; Page 30; 162pp; English.
 XX The invention relates to methods for the screening, diagnosis and
 CC prognosis of Alzheimer's disease. The methods involve the detection
 CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
 CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
 CC serum or plasma. The abundance of the AFs and APIs is then
 CC normalised to an Expression Reference Protein Isoform (ERPI) in
 CC order to determine whether a patient is suffering from, or has
 CC a predisposition to, Alzheimer's Disease. The relative abundance of
 CC the AFs and APIs correlates with the severity of Alzheimer's Disease.
 CC The present sequence is a peptide produced from an API by proteolysis.

SQ Sequence 7 AA;

Query Match 60.6%; Score 20; DB 22; Length 7;
 Best Local Similarity 57.1%; Pred. No. 9.3e+05;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy i FTUKISR 7
 Db : : : : :
 i FTPEYSR 7

RESULT 12
 ABB52355
 ID ABB52355 standard; Peptide; 7 AA.
 XX
 AC ABB52355;
 XX
 DT 08-FEB-2002 (first entry)
 XX
 DE Human API-125 tryptic digest peptide #8.
 XX
 KW Human; neuroprotective; nontopic; gene therapy; vaccine;
 KW Alzheimer's Disease; Alzheimer's Disease-Associated Feature; AF;
 KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
 KW Expression Reference Protein Isoform; ERPI; proteolysis.
 XX
 OS Homo sapiens.
 XX
 PN WO200175454-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 03-APR-2001; 2001WO-US10908.
 XX
 PR 03-APR-2000; 2000US-194504P.
 PR 28-NOV-2000; 2000US-253647P.
 XX
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA (PFIZ) PFIZER INC.

Durham KL, Friedman DL, Horath HMAc, Kimmel LH, Parekh RB;
 Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;
 Townsend RR, White F, Williams SA;
 WPI; 2001-639384/73.
 Screening for Alzheimer's disease in a mammal, by making
 two-dimensional array of a feature whose relative abundance correlates
 with disease, and comparing with abundance of the feature in samples of
 healthy persons

Example; Page 34; 162pp; English.
 The invention relates to methods for the screening, diagnosis and
 CC prognosis of Alzheimer's disease. The methods involve the detection
 CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
 CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
 CC serum or plasma. The abundance of the AFs and APIs is then
 CC normalised to an Expression Reference Protein Isoform (ERPI) in
 CC order to determine whether a patient is suffering from, or has

CC a predisposition to, Alzheimer's Disease. The relative abundance of
 CC the Afs and APIs correlates with the severity of Alzheimer's Disease.
 CC The present sequence is a peptide produced from an API by proteolysis.
 XX
 SQ Sequence 7 AA;

Query Match 60.6%; Score 20; DB 22; Length 7;
 Best Local Similarity 42.9%; Pred. No. 9.3e+05;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
 :||:|
 Db 1 YTFELSR 7

RESULT 13
 AAU28602
 ID AAU28602 standard; Peptide; 7 AA.

XX AC AAU28602;

XX DT 03-JAN-2002 (first entry);

XX DE DPI tryptic digest peptide #133.

XX KW Human; depression associated protein isoform; tryptic digest peptide;
 XX DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
 XX KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
 XX KW maniac-depressive illness; schizoaffective disorder.

XX OS Homo sapiens.

XX PN WC200162787-A1.

XX PD 30-AUG-2001.

XX PF 23-FEB-2001; 2001WO-GB00786.

XX PR 24-FEB-2000; 2000GB-0004412.

XX PR 08-DEC-2000; 2000GB-0030050.

XX PR 12-DEC-2000; 2000US-0254830.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

XX DR WPI; 2001-570626/64.

XX PT Novel nucleic acid encoding a protein associated with bipolar affective
 XX disorder, which is used for diagnosis, prophylaxis and therapy of
 XX neuropsychiatric disorders, such as bipolar affective disorder -

XX PS Disclosure; Page 34; 153pp; English.

XX CC The present invention relates to the identification of depression
 XX associated protein isoforms (DPIs), particularly the tryptic digest
 XX peptides of these proteins. Some of the DPIs (AAU28404-AAU28625;
 XX described are decreased in the cerebrospinal fluid (CSF) of BAD
 XX (bipolar affective disorder) subjects, whilst other DPIs
 XX (AAU28626-AAU2887) are increased in BAD subjects. Also described
 XX are peptide sequences identified from DPI-45 and DPI-213 and the
 XX nucleic acid sequences they are encoded by. The sequences of the
 XX invention are useful for clinical screening, diagnosis, prognosis,
 XX therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also
 XX known as bipolar mood disorder, BP), maniac-depressive illnesses,
 XX attention deficit disorders, schizoaffective disorders, and unipolar
 XX affective disorders. The present sequence represents one of the DPI
 XX tryptic digest peptides of the present invention.

XX Sequence 7 AA;

Query Match 60.6%; Score 20; DB 22; Length 7;
 Best Local Similarity 42.9%; Pred. No. 9.3e+05;

Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FTLKISR 7
 :||:|
 Db 1 YTFELSR 7

RESULT 14

AAU24969
 ID AAU24969 standard; Peptide; 7 AA.

XX AC AAU24969;

XX DT 18-DEC-2001 (first entry)

XX DE Schizophrenia-Associated Protein Isoform (SPI) peptide #196.

XX KW Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;
 XX KW neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.

XX OS Homo sapiens.

XX PN WC200162785-A2.

XX PD 30-AUG-2001.

XX PF 23-FEB-2001; 2001WO-GB00792.

XX PR 24-FEB-2000; 2000GB-0004415.

XX PR 28-NOV-2000; 2000US-0750395.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

XX DR WPI; 2001-570624/64.

XX CC New schizophrenia associated protein isoforms and encoding nucleic acid
 XX molecules, useful for treatment, diagnosis and prognosis of
 XX schizophrenia and screening for potential drugs for treatment and new
 XX drug targets -

XX PS Disclosure; Page 32; 148pp; English.

XX CC The sequence represents a schizophrenia-associated protein isoform (SPI).
 XX These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
 XX in cerebrospinal fluid, serum or plasma and are useful markers of
 XX schizophrenia. The sequences can be used for treatment and diagnosis of
 XX schizophrenia, screening, prognosis, monitoring the results of therapy,
 XX identifying patients most likely to respond to a particular therapy and
 XX identification of new targets for drug treatment. SPI DNA is useful as a
 XX nucleic acid probe to detect the presence of nucleic acids or SPIs.

XX Sequence 7 AA;

Query Match 60.6%; Score 20; DB 22; Length 7;
 Best Local Similarity 42.9%; Pred. No. 9.3e+05;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
 :||:|
 Db 1 YTFELSR 7

RESULT 15

AAU26249
 ID AAU26249 standard; Peptide; 7 AA.

XX AC AAU26249;

XX DT 18-DEC-2001 (first entry)

XX DE Depression-Associated Protein isoform DPI-208.

XX Human; Bipolar Affective Disorder; BAD; Depression-Associated Feature;
KW Df; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;
KW CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;
KW attention deficient disorder; schizoaffective disorder;
KW unipolar affective disorder.
XX OS Homo sapiens.
XX PN WO200163294-A2.
XX PD 30-AUG-2001.
XX 23-FEB-2001; 2001WO-0500751.
XX 24-FEB-2000; 2000GB-0004412.
PR 08-DEC-2000; 2000GB-0010850.
PR 12-DEC-2000; 2000US-0254830.
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PA Herath HMAC, Parekh RB, Rohlf C;
PI WI; 2001-582081/65.
XX DR
XX
XX Preparation for diagnosing or treating bipolar affected disorder (BAD;
PT or unipolar depression, or for screening for modulators, comprises a
PT BAD-associated protein isoform -
XX
XX Claim 8; Page 34; 163pp; English.
XX
XX The invention relates to a preparation comprising an isolated Bipolar
CC Affected Disorder (BAD)-Associated Protein Isoform (DPI's). The DPI's are
CC used to screen, diagnose or prognosis of BAD or unipolar depression,
CC determine the stage or severity of BAD or unipolar depression, identify a
CC subject at risk of developing BAD or unipolar depression, or monitor the
CC effect of therapy in a subject. They are also used to screen for or
CC identify agents that interact with a DPI. These agents, antibodies
CC against the DPIs, and nucleic acids encoding the DPIs are used to treat
CC or prevent BAD or unipolar depression. Diseases that can be treated are
CC attention deficient disorder, a schizoaffective disorder, a bipolar or a
CC unipolar affective disorder. The DPIs are used in proteomics. The
CC proteomic approach of using DPIs for screening, diagnosis or prognosis of
CC BAD or unipolar depression overcomes the problems of using gene
CC expression analysis, such as not being able to obtain central nervous
CC system (CNS) tissue from a living patient under normal circumstances.
CC The present sequence is a DPI decreased in the CSF (cerebro-spinal
CC fluid) of subjects having BAD.
XX
SQ Sequence 7 AA;
Query Match 60.6%; Score 20; DB 22; Length 7;
Best Local Similarity 42.9%; Pred. No. 9.3e+55;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 FTLKISR 7
Db 1 YTEPLSR 7

Search completed: October 4, 2003, 12:45:24
Job time : 52.6667 secs

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OM protein - protein search, using sw model

Run on: October 4, 2003, 12:48:43 ; Search time 33.6667 Seconds
(without alignments)
32.896 Million cell updates/sec

Title: US-09-712-819C-6

Perfect score: 33

Sequence: 1 FTUKISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 587654 seqs, 159212981 residues

Total number of hits satisfying chosen parameters: 33362

Minimum DB seq length: 0

Maximum DB seq length: ?

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	60.6	7	10	US-09-791-378-198
2	20	60.6	7	10	US-09-998-909-7
3	20	60.6	7	10	US-09-826-290-205
4	20	60.6	7	10	US-09-826-290-370
5	20	60.6	7	10	US-09-791-393-145
6	20	60.6	7	10	US-09-791-389-145
7	18	54.5	7	10	US-09-996-288-164
8	18	54.5	7	10	US-09-996-265-164
9	18	54.5	7	10	US-10-162-497-78
10	17	51.5	6	15	US-10-105-930-39
11	17	51.5	6	15	US-10-043-539-39
12	17	51.5	7	10	US-09-996-288-135
13	17	51.5	7	11	US-09-996-265-135
14	17	51.5	7	14	US-10-044-034-13
15	16	48.5	6	10	US-09-727-963A-88

16	48.5	6	15	US-10-211-994-23	Sequence 23, Appl1
17	48.5	7	9	US-09-989-789-396	Sequence 396, App
18	48.5	7	9	US-09-989-789-1971	Sequence 1971, Ap
19	48.5	7	9	US-09-989-789-3503	Sequence 3503, Ap
20	48.5	7	9	US-09-989-789-3542	Sequence 3542, Ap
21	48.5	7	9	US-09-989-789-3544	Sequence 3544, Ap
22	48.5	7	9	US-09-796-848A-2C	Sequence 20, Appl1
23	48.5	7	10	US-09-844-508-43	Sequence 43, Appl1
24	48.5	7	10	US-09-848-387-44	Sequence 44, Appl1
25	48.5	7	10	US-09-996-288-35	Sequence 35, Appl1
26	48.5	7	10	US-09-996-288-96	Sequence 96, Appl1
27	48.5	7	10	US-09-996-288-131	Sequence 131, App
28	48.5	7	11	US-09-990-186-396	Sequence 396, App
29	48.5	7	11	US-09-990-186-1971	Sequence 1971, Ap
30	48.5	7	11	US-09-990-186-3523	Sequence 3523, Ap
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32	48.5	7	11	US-09-990-186-3544	Sequence 3544, Ap
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34	48.5	7	11	US-09-996-265-96	Sequence 96, Appl1
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36	48.5	7	11	US-09-989-994-396	Sequence 396, App
37	48.5	7	11	US-09-989-994-1971	Sequence 1971, Ap
38	48.5	7	11	US-09-989-994-3503	Sequence 3503, Ap
39	48.5	7	11	US-09-989-994-3542	Sequence 3542, Ap
40	48.5	7	11	US-09-989-994-3544	Sequence 3544, Ap
41	48.5	7	14	US-10-050-552A-4	Sequence 4, Appl1
42	48.5	7	15	US-10-084-926-43	Sequence 43, Appl1
43	48.5	7	15	US-10-214-026-6	Sequence 6, Appl1
44	45.5	4	12	US-10-348-167-36	Sequence 36, Appl1
45	45.5	5	12	US-10-288-186-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1

US-09-791-378-198
; Sequence 198, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-198

Query Match 60.6%; Score 20; DB 10; Length 7;
Best Local Similarity 42.9%; Pred. No. 5.2e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTUKISR 7

Dh 1 YTELSR 7

RESULT 2

US-09-998-909-7
; Sequence 7, Application US/09998909
; Patent No. US20020164664A1
; GENERAL INFORMATION:
; APPLICANT: Hlavaty, John
; APPLICANT: Briggman, Joseph
; TITLE OF INVENTION: Detection and Treatment of Prostate Cancer

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; FILE REFERENCE: NTP-027
; CURRENT APPLICATION NUMBER: US/09/999,909
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/250,284
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-998-909-7

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Query Match      60.6%; Score 20; DB 10; Length 7;
Best Local Similarity 42.9%; Pred. No. 5.2e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 FTLKISR 7
   :|::||
Db 1 YTFELSR 7

```

```

RESULT 3
US-09-826-290-205
; Sequence 205, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Dutham, L. Kathryn
; APPLICANT: Friedmann, David L.
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Shikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlff, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-205

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Query Match      60.6%; Score 20; DB 10; Length 7;
Best Local Similarity 57.1%; Pred. No. 5.2e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 FTLKISR 7
   :|::||
Db 1 YTFEYSR 7

```

```

RESULT 4
US-09-826-290-370
; Sequence 370, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Dutham, L. Kathryn

```

```

; APPLICANT: Friedmann, David L.
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Shikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlff, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 370
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-370

```

```

Query Match      60.6%; Score 20; DB 10; Length 7;
Best Local Similarity 42.9%; Pred. No. 5.2e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 FTLKISR 7
   :|::||
Db 1 YTFELSR 7

```

```

RESULT 5
US-09-791-393-145
; Sequence 145, Application US/09791393
; Publication No. US20030032209A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Shikhu
; APPLICANT: Rohlff, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAP)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0003050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,630
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-145

```

```

Query Match      60.6%; Score 20; DB 11; Length 7;
Best Local Similarity 42.9%; Pred. No. 5.2e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 FTLKISR 7
   :|::||

```

Db 1 YTFELSR 7

RESULT 6

US-09-791-389-145
; Sequence 145, Application US/09791389
; Publication No. US2003032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Ronliff, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GH 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GR 9030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 59/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-791-389-145

Query Match 60.8%; Score 20; DB 11; Length 7;
Best Local Similarity 42.9%; Pred. No. 5.2e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
|:|:|
Db 1 YTFELSR 7

RESULT 7

US-09-996-288-164
; Sequence 164, Application US/09996288
; Patent No. US2002017726A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2002-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-164

Query Match 54.5%; Score 18; DB 12; Length 7;
Best Local Similarity 60.8%; Pred. No. 5.2e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLKIS 6
|:|:|
Db 2 TMKLS 6

RESULT 8

US-10-105-930-39

; Sequence 39, Application US/10105930

US-09-996-265-164
; Sequence 164, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-164

Query Match 54.5%; Score 18; DB 12; Length 7;
Best Local Similarity 60.8%; Pred. No. 5.2e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLKIS 6
|:|:|
Db 2 TMKLS 6

RESULT 9

US-10-162-497-78
; Sequence 78, Application US/10162497
; Publication No. US20030158398A1
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Feinberg, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CHROMOSOME-14P RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/10/162,497
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US/09/657,474
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 09/268,992
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/088,312
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-497-78

Query Match 54.5%; Score 18; DB 12; Length 7;
Best Local Similarity 50.8%; Pred. No. 5.2e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLKIS 6
|:|:|
Db 2 YTMKIS 7

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; Publication No. US20030009012A;
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; TITLE OF INVENTION: NOVEL HEMOPHILIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105J5;
; CURRENT APPLICATION NUMBER: US/10/105,930
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JPC/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-39

Query Match 51.5%; Score 17; DB 15; Length 6;
Best Local Similarity 60.0%; Pred. No. 5.2e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 1 FTLXI 5
Db 1 YTCQI 5

RESULT 11
US-10-043-539-30
; Sequence 30, Application US/10043539
; Publication No. US20030114650A;
; GENERAL INFORMATION:
; APPLICANT: Cheung, Ambrose
; APPLICANT: Zhang, Gongyi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN
; FILE REFERENCE: DC-0199
; CURRENT APPLICATION NUMBER: US/10/043,539
; CURRENT FILING DATE: 2002-01-11
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,233
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,607
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/289,621
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-043-539-30

Query Match 51.5%; Score 17; DB 15; Length 6;
Best Local Similarity 60.0%; Pred. No. 5.2e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 3 LKISR 7
Db 2 IKTR 6

RESULT 12
US-09-996-288-135
; Sequence 135, Application US/C0996288
; Patent No. US2002017126A;
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-135

Query Match 51.5%; Score 17; DB 10; Length 7;
Best Local Similarity 60.0%; Pred. No. 5.2e-05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 2 TLKIS 6
Db 2 TLKLA 6

RESULT 13
US-09-996-265-135
; Sequence 135, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/C09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-135

Query Match 51.5%; Score 17; DB 11; Length 7;
Best Local Similarity 60.0%; Pred. No. 5.2e-05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 2 TLKIS 6
Db 2 TLKLA 6

RESULT 14
US-10-044-034-13
; Sequence 13, Application US/10044034
; Publication No. US20020169264A;
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DAVID C.
; APPLICANT: O'BRIEN-SIMPSON, NEIL M.
; APPLICANT: BROWN, LORENA E.
; APPLICANT: EDE, NICHOLAS J.
; APPLICANT: BRANDT, EVELYN R.
; APPLICANT: GOOD, MICHAEL F.
; TITLE OF INVENTION: POLYMERS INCORPORATING PEPTIDES
; FILE REFERENCE: FBRC-006
; CURRENT APPLICATION NUMBER: US/10/044,034
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: P05071
; PRIOR FILING DATE: 1997-02-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
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SEQ ID NO 13

LENGTH: 7

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptides

JS-10-044-034-13

Query Match

51.5%; Score 17; DB 14; Length 7;

Best Local Similarity

60.0%; Pred. No. 5.2e+05;

Matches 3; Conservative

2; Mismatches 0; Indels 0; Gaps 0;

2Y 2 TLKIS 6

1 1 1 1 1 1

1b 1 TLKLA 5

RESULT 15

S-09-727-963A-88

Sequence 88, Application JS/09727963A

Patent No. US20020155106A1

GENERAL INFORMATION:

APPLICANT: V.I. Technologies, Inc.

APPLICANT: Hammond, David J.

TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE

FILE REFERENCE: 18242-505

CURRENT APPLICATION NUMBER: US/09/727,963A

CURRENT FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557

PRIOR FILING DATE: 1999-12-02

NUMBER OF SEQ ID NOS: 99

SOFTWARE: PatentIn ver. 2.1

SEQ ID NO 88

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Peptide Ligand

NAME/KEY: VARIANT

LOCATION: (1)

OTHER INFORMATION: wherein Xaa is D-phenylalanine

JS-09-727-963A-88

Query Match

48.5%; Score 16; DB 10; Length 6;

Best Local Similarity

75.0%; Pred. No. 5.2e+05;

Matches 3; Conservative

0; Mismatches 1; Indels 0; Gaps 0;

2Y 1 FTLK 4

1 1 1 1 1 1

1b 3 FTFK 6

Search completed: October 4, 2003, 13:05:05

Ob time : 34.6667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

M protein - protein search, using sw model

run on: October 4, 2003, 12:42:47 ; Search time 17 Seconds
(without alignments)
17,422 Million cell updates/sec

title: US-09-712-819C-6

effect score: 33

equences: 1 FTLKISR 7

coring table: BLCSUM62

Gapop 10.0 , Gapext 0.5

searched: 328717 seqs, 42110858 residues

total number of hits satisfying chosen parameters: 43738

inimum DB seq length: 0

aximum DB seq length: 7

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database :

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.rep.*
3: /cgn2_6/ptodata/1/1aa/5A_COMB.rep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.rep.*
5: /cgn2_6/ptodata/1/1aa/6CTUS_COVA.rep.*
6: /cgn2_6/ptodata/1/1aa/6ackf1.esl.rep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length DB	ID	Description
1	20	60.6	7	5	US-08-222-619-8
2	20	60.6	7	5	PCT-US95-04075-8
3	19	57.6	6	6	5252328-8
4	18	54.5	7	2	US-08-346-333-24
5	18	54.5	7	4	US-08-288-932-78
6	18	54.5	7	4	US-09-657-474-78
7	18	54.5	7	5	PCT-US91-07506-24
8	17	51.5	7	2	US-08-174-060-17
9	17	51.5	7	3	US-08-654-623-63
10	17	51.5	7	3	US-08-338-382-17
11	16	48.5	5	3	US-08-591-632-23
12	16	48.5	5	4	US-07-717-331F-5
13	16	48.5	6	2	US-07-717-331F-5
14	16	48.5	6	4	US-08-757-425B-44
15	16	48.5	7	1	US-07-634-641-12
16	16	48.5	7	1	US-08-136-743B-55
17	16	48.5	7	3	US-09-043-216-28
18	16	48.5	7	3	US-09-173-941-72
19	16	48.5	7	4	US-09-423-468A-6
20	16	48.5	7	4	US-08-756-223A-26
21	15	45.5	4	4	US-08-305-571A-17
22	15	45.5	4	4	US-08-788-822A-1
23	15	45.5	4	4	US-08-134-23C-26
24	15	45.5	5	1	US-08-136-743B-63
25	15	45.5	5	3	US-09-040-216-55
26	15	45.5	5	3	US-08-591-632-17
27	15	45.5	5	3	US-08-591-632-26

Sequence 17, Appl
Sequence 26, Appl
Sequence 62, Appl
Sequence 6, Appl
Sequence 4, Appl
Sequence 21, Appl
Sequence 41, Appl
Sequence 6, Appl
Sequence 41, Appl
Sequence 6, Appl
Sequence 41, Appl
Sequence 219, Appl
Sequence 54, Appl
Sequence 6, Appl
Sequence 41, Appl
Sequence 219, Appl
Sequence 650, Appl

ALIGNMENTS

RESULT 1
US-08-222-619-8
; Sequence 8, Application US/05222619
; Patent No. 5652352
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri
; APPLICANT: Lyons, David
; APPLICANT: Wurfel, Mark
; APPLICANT: Wright, Samuel
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Angen Center, Patent Operations/RKC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/222,619
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-222-619-8

Query Match 60.6%; Score 20; DB 1; Length 7;
Best Local Similarity 57.1%; Pred. No. 2.5e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
Db 1 FTPEYSR 7

RESULT 2
PCT-US95-04075-8
; Sequence 8, Application PC/TUS9504075
; GENERAL INFORMATION:

APPLICANT: AMGEN INC.
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Center, Patent Operations/ERC
STREET: 1840 Delaville and Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: U.S.
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04075
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-04075-8

Query Match 60.6%; Score 20; DB 5; Length 7;
Best Local Similarity 57.1%; Pred. No. 2.5e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

2Y 1 FTLKISR 7
db 1 PTFEYSR 7

RESULT 3

252328-8
Patent No. 5252328
APPLICANT: FAULDS, DARYL; VISHOOT, NIMI; BROCKS, EMILY
TITLE OF INVENTION: MYOPLASMA HYOPNEUMONIAE ANTIGEN AND USES
THEREFORE

NUMBER OF SEQUENCES: 15
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/335,726
FILING DATE: 07-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 30,130
FILING DATE: 26-MAR-1987
SEQ ID NO: 8:
LENGTH: 6

252328-8
Query Match 57.6%; Score 17; DB 6; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2Y 1 FTLKI 5
db 2 FVLKI 6

RESULT 4

US-C8-346-333-24
Sequence 24, Application: US/05346333
Patent No. 5677153
GENERAL INFORMATION:
APPLICANT: Botstein, David
APPLICANT: Palzkill, Timothy
TITLE OF INVENTION: Methods for modifying DNA and for
TITLE OF INVENTION: detecting effects of such modification on interaction of

TITLE OF INVENTION: encoded modified polypeptides with target substrates.
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,333
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/339,501
FILING DATE:
APPLICATION NUMBER: US 07/602,159
FILING DATE: 22-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,601
REFERENCE/DOCKET NUMBER: A-53469/RFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-C8-346-333-24

Query Match 54.5%; Score 18; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKI 5
db 2 TLKI 5

RESULT 5

US-09-268-992-78
Sequence 78, Application US/09268992
Patent No. 6342351
GENERAL INFORMATION:
APPLICANT: Chen, H.
APPLICANT: Preimer, N.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
FILE REFERENCE: 7853-138
CURRENT APPLICATION NUMBER: US/39/268,992
CURRENT FILING DATE: 1999-03-16
EARLIER APPLICATION NUMBER: 09/236,134
EARLIER FILING DATE: 1999-01-22
EARLIER APPLICATION NUMBER: 60/106,056
EARLIER FILING DATE: 1998-10-28
EARLIER APPLICATION NUMBER: 60/089,312
EARLIER FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 60/079,044
EARLIER FILING DATE: 1998-03-16
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 78
LENGTH: 7
TYPE: PRT

ORGANISM: Homo sapiens

S-09-268-992-73

Query Match 54.5%; Score 18; DB 4; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.5e+25;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Y 1 FTLKIS 6
b 2 YTMKYS 7

RESULT 6

S-09-657-474-78

Sequence 78, Application US/09657474

Patent No. 6399762

GENERAL INFORMATION:

APPLICANT: Chen, H.

APPLICANT: Freimer, N.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS

FILE REFERENCE: 7853-138

CURRENT APPLICATION NUMBER: US/09/657,474

CURRENT FILING DATE: 2800-09-07

PRIOR APPLICATION NUMBER: 09/268,392

PRIOR FILING DATE: 1999-03-16

PRIOR APPLICATION NUMBER: 09/236,134

PRIOR FILING DATE: 1999-01-22

PRIOR APPLICATION NUMBER: 60/106,056

PRIOR FILING DATE: 1998-10-28

PRIOR APPLICATION NUMBER: 60/088,312

PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/078,344

PRIOR FILING DATE: 1998-03-16

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 78

LENGTH: 7

TYPE: PRT

ORGANISM: Homo sapiens

S-09-657-474-78

Query Match 54.5%; Score 18; DB 4; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.5e+25;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Y 1 FTLKIS 6
b 2 YTMKYS 7

RESULT 7

CT-US91-07506-24

Sequence 24, Application PC/TUS9107506

GENERAL INFORMATION:

APPLICANT: Botstein, David

APPLICANT: Palzkill, Timothy

TITLE OF INVENTION: Methods for modifying DNA and for

TITLE OF INVENTION: detecting effects of such modification on interaction of

TITLE OF INVENTION: encoded modified polypeptides with target substrates.

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Richard F. Treacartin

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/07506

FILING DATE: 1991021

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Treacartin, Richard F.

REGISTRATION NUMBER: 31,801

REFERENCE/DOCKET NUMBER: EP-53469-PC/PTT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US91-07506-24

Query Match 54.5%; Score 18; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.5e+25;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKI 5
DB 2 TLKI 5

RESULT 8

US-09-174-060-17

Sequence 17, Application US/09174060

Patent No. 5989554

GENERAL INFORMATION:

APPLICANT: Knuth, Mark W

APPLICANT: Haak-Frendscho, Mary

APPLICANT: Shultz, John W

APPLICANT: Lesley, Scott A

APPLICANT: Villars, Catherine E

TITLE OF INVENTION: HIGH LEVEL EXPRESSION AND FACILE

TITLE OF INVENTION: PURIFICATION OF PROTEINS, PEPTIDES AND CONJUGATES FOR

TITLE OF INVENTION: IMMUNIZATION, PURIFICATION AND DETECTION APPLICATIONS

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ross & Stevens, S.C.

STREET: 1 South Pinckney St.

CITY: Madison

STATE: WI

COUNTRY: USA

ZIP: 53701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/174,060

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/338,382

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Sata, Charles S

REGISTRATION NUMBER: 30,492

REFERENCE/DOCKET NUMBER: 34506.024

TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-257-5353

TELEFAX: 608-257-9175

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS: UNKNOWN
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-174-060-17

Query Match 51.5%; Score 17; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTJK 4
:|:|:
Db 1 YTLK 4

RESULT 9

US-08-654-623-69
Sequence 69, Application US/09654623
Patent No. 601084
GENERAL INFORMATION:
APPLICANT: Griffiths, Andrew D
APPLICANT: Holliger, Kaspar-Philipp
APPLICANT: Nissim, Ahuva
APPLICANT: Fisch, Igor
APPLICANT: Wichter, Gregory F
TITLE OF INVENTION: Recombinant Binding Proteins and Peptides
NUMBER OF SEQUENCES: 7;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gershtein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO);
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/654,623

FILING DATE: 29-MAY-1996
CLASSIFICATION: 435
CLASSIFICATION: C12N 1/21, C12R 1:19)

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9225453.1

FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9300816.7

FILING DATE: 16-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 930336.4.7

FILING DATE: 10-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9315969.3

FILING DATE: 22-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02492

FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9412147.2

FILING DATE: 17-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/02662

FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 03/448,418

FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough

REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33259
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-654-623-69

Query Match 51.5%; Score 17; DB 3; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKIS 6
:|:|:
Db 1 SLKVS 5

RESULT 10

US-08-338-382-17
Sequence 17, Application US/08338382
Patent No. 6069230
GENERAL INFORMATION:

APPLICANT: Knuth, Mark W
APPLICANT: Haak-Frendscho, Mary
APPLICANT: Shultz, John W
APPLICANT: Lesley, Scott A
APPLICANT: Villars, Catherine E
TITLE OF INVENTION: HIGH LEVEL EXPRESSION AND FACILE
TITLE OF INVENTION: PURIFICATION OF PROTEINS, PEPTIDES AND CONJUGATES FOR
TITLE OF INVENTION: IMMUNIZATION, PURIFICATION AND DETECTION APPLICATIONS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:

ADDRESSEE: Ross & Stevens, S.C.
STREET: 1 South Pinckney St.
CITY: Madison
STATE: WI
COUNTRY: USA

ZIP: 53701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/338,382
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Sara, Charles S
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 34506,024
TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-257-5353
TELEFAX: 608-257-9175
INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: unknown

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-338-382-17

Query Match 51.5%; Score 17; DB 3; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTJK 4
:|:|:
Db 1 YTLK 4

RESULT 11

S-08-591-632-23
Sequence 23, Application US/08591632
Patent No. 6261538
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10350 No. 6261558th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,632
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11907
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSI 332.3
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match 48.5%; Score 16; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.5e-05;
Matches 3; Conservative 1; Mismatches 0; Indels 0;
Gaps 0;
1 FTLQ 4
2 FTLQ 5
-08-591-632-23

RESULT 12
-09-611-451-23
Sequence 23, Application US/09611451
Patent No. 6395275
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Burton, Dennis R.
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10350 No. 6261558th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10350 No. 6395275th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSI 332.3
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-611-451-23

Query Match 48.5%; Score 16; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.5e-05;
Matches 3; Conservative 1; Mismatches 0; Indels 0;
Gaps 0;
1 FTLK 4
2 FTLQ 5
Db

RESULT 13
US-07-717-331F-5
Sequence 5, Application US/07717331F
Patent No. 5484905
GENERAL INFORMATION:
APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua
APPLICANT: Stein
TITLE OF INVENTION: A Receptor Protein Kinase Gene
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
ZIP: 06611
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/717,331F
FILING DATE: June 19th 1991
CLASSIFICATION: 80C
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yawwak
REGISTRATION NUMBER: 26,824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-717-331F-5

Query Match 48.5%; Score 16; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Y 3 LKVS 6
b 2 LKVS 5

RESULT 14
US-08-757-425B-44
Sequence 44, Application US/08/757425B
Patent No. 6500660
GENERAL INFORMATION:
APPLICANT: Pastrez, Jacques
TITLE OF INVENTION: Chimeric Target Molecules Having A Regulatable Activity
FILE REFERENCE: 100350-09643
CURRENT APPLICATION NUMBER: US/08/757.425B
CURRENT FILING DATE: 1996-11-27
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn version 3.1
SEQ ID NO 44
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Mimetope
US-08-757-425B-44

Query Match 45.5%; Score 16; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Y 2 LKVS 6
b 2 LKVS 6

RESULT 15
US-07-634-641-12
Sequence 12, Application US/07634641
Patent No. 5386011
GENERAL INFORMATION:
APPLICANT: Wiedeman, Paul E.
APPLICANT: Kawai, Megumi
APPLICANT: Luly, Jay R.
APPLICANT: Or, Yat-Sun
TITLE OF INVENTION: Hexa- and Heptapeptide Anaphylatoxin
TITLE OF INVENTION: Receptor Ligands
NUMBER OF SEQUENCES: 2;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: No. 5386011th Chicago
STATE: IL

COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.125
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,641
FILING DATE: 19901227
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Janssen, Jerry F.
REGISTRATION NUMBER: 29,175
REFERENCE/DOCKET NUMBER: 4934.JS.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 937-4558
TELEFAX: (708) 937-9556
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-641-12
Query Match 48.5%; Score 15; DB 1; Length 7;
Best Local Similarity 28.6%; Pred. No. 2.5e+05;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Y 1 PTLK-SR 7
b 1 FAMRLGR 7
Search completed: October 4, 2003, 12:50:35
Job time : 19 secs